

From: Whiteman, Brian
Sent: Monday, August 29, 2005 4:04 PM
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Subject: seq search

09/801,371

SEQ ID NO: 1 and 2

1) the commercial databases, and the issued and published US application databases

Thank you,

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: *8/1/05*
Date Completed: *8/8/05*
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: *2* AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *10311*
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: September 2, 2005, 18:55:28 ; Search time 1896.05 Seconds

(without alignments)
 2657.805 Million cell updates/sec

Title: US-09-801-371A-1
 Perfect score: 104

Sequence: 1 gaattcaaacctggggccatcc.....99ttctggccagaatgcgtgc 104

Scoring table: IDENTITY_NUC
 Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
 1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

RESULT 1
 G13533

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

STS.

Homo sapiens (human)

Homo sapiens

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 400)

Olivier, M. and Cox, D.R.

Unpublished, Olivier, M., Cox, D.R. (2000)

Olivier, M. and Cox, D.R.

Unpublished (2000)

ALIGNMENTS

X01394 Human mRNA
 BC028148 Homo sapi
 BD137687 Self-regu
 AR30459 Sequence
 BD137688 Self-regu
 AR30460 Sequence
 M26331 Human tumor
 AR100270 Sequence
 AR149925 Sequence
 BD227798 Antisense
 BD271232 Predictio
 BD064008 Novel exp
 X02910 Human gene
 AY066019 Homo sapi
 AB088112 Homo sapi
 AX100950 Sequence
 AX100965 Sequence
 M16441 Human tumor
 AY214167 Homo sapi
 AR562497 Sequence
 Z15026 Homo sapien
 BX248519 Human DNA
 AL929587 Human DNA
 Y14768 Homo sapien
 AP000505 Homo sapi
 BX927320 Human DNA

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	400	11 G13533	G13533 SHGC-11076
2	104	100.0	787	6 BD137681	BD137681 Self-regu
3	104	100.0	787	6 AR300453	AR300453 Sequence
4	104	100.0	787	6 BD070551	BD070551 Self-regu
5	104	100.0	1275	6 I08430	I08430 Sequence 5
6	104	100.0	1323	6 I07953	I07953 Sequence 6
7	104	100.0	1324	6 E00702	E00702 cDNA encodi
8	104	100.0	1324	6 I03610	I03610 Sequence 2
9	104	100.0	1465	6 I04244	I04244 Sequence 2
10	104	100.0	1585	6 A37272	A37272 Sequence 12
11	104	100.0	1585	6 I04169	I04169 Sequence 1
12	104	100.0	1585	6 I04198	I04198 Sequence 1
13	104	100.0	1585	6 I08384	I08384 Sequence 5
14	104	100.0	1585	6 I08429	I08429 Sequence 3
15	104	100.0	1585	6 AR380784	AR380784 Sequence
16	104	100.0	1585	9 HUMTNFAA	M10988 Human tumor
17	104	100.0	1606	6 I07541	I07541 Sequence 22
18	104	100.0	1643	6 AR146199	AR146199 Sequence
19	104	100.0	1643	6 AR366225	AR366225 Sequence

Buffer:

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/uL

Total Vol: 10 uL

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

MgCl₂: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from M10988 -- Unigene.

FEATURES	source	Location/Qualifiers
1. .400	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /map="6" /clone.lib="Human" 210. .375 210. .231 complement(356. .375)	

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Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTGACATCTG 60
Db 216 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTGACATCTG 275

Qy 61 GAATCTGGAGAACCGGAGCTTTGGTTCTGGCCAGGAATGCTGC 104
Db 276 GAATCTGGAGAACCGGAGCTTTGGTTCTGGCCAGGAATGCTGC 319

RESULT 2
BD137681 LOCUS BD137681 787 bp DNA linear PAT 18-SEP-2002
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION BD137681.1 GI:23232626
VERSION JP 2002504381-A/7.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 787)
Tatake, R.J.; Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: JP 2002504381-A 7 12-FEB-2002;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002504381-A/7
PD 12-FEB-2002
PF 12-JAN-1999 JP 2000533579
PR 27-FEB-1998 US 60/076316
PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC
C12N15/09, A61K31/7088, A61K48/00, A61P1/04, A61P3/10, A61P17/06, PC
A61P25/00, PC A61P29/00, A61P43/00, C12N9/64, C12Q1/68//C12N5/10, C12N15/00, PC
C12N5/00
CC TNF-alpha untranslated region
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FT source 1. .787
/organism='Homo sapiens (human)' .
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source

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Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTGACATCTG 60

Db 222 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTGACATCTG 281
Qy 61 GAATCTGGAGAACCGGAGCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 282 GAATCTGGAGAACCGGAGCTTTGGTTCTGGCCAGAAATGCTGC 325

RESULT 3
AR300453 LOCUS AR300453 787 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7 from patent US 6537784.
ACCESSION AR300453
VERSION AR300453.1 GI:31687895
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 787)
AUTHORS Tatake, R.J., Marlin, S.D. and Barton, R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: US 6537784-A 7 25-MAR-2003;
FEATURES Location/Qualifiers
source 1. .787
/organism="unknown"
/mol_type="genomic DNA"

Query Match 100.0%; Score 104; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTGACATCTG 60
Db 222 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTGACATCTG 281

RESULT 4
BD070551 LOCUS BD070551 787 bp DNA linear PAT 27-AUG-2002
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION BD070551
VERSION BD070551.1 GI:22616154
KEYWORDS JP 2001516210-A/13.
SOURCE unidentified
ORGANISM unidentified
Unclassified.

REFERENCE 1 (bases 1 to 787)
AUTHORS Tatake, R.J., Marlin, S.D. and Barton, R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: JP 2001516210-A 13 25-SEP-2001;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
COMMENT OS unidentified
PN JP 2001516210-A/13
PD 25-SEP-2001
PF 27-FEB-1998 JP 1998537909
PR 28-FEB-1997 US 60/039266
PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC
A61K31/70, C07H21/04, C12N15/12, C12P19/34
CC Strandedness: Single;
CC Topology: Linear;
CC TNF alpha nontranslated region
FH Key Location/Qualifiers
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/organism="Unidentified".
1. .787
/organism="Unidentified".
FT Location/Qualifiers
source 1. .787
/organism="unidentified"
/mol_type="genomic DNA"

ORIGIN /db_xref="taxon:32644"

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Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 222 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG 281

Qy 61 GAATCTGGAGACCAGGGAGCCTTGGTTCTGCCAGAATGCTGC 104
Db 282 GAATCTGGAGACCAGGGAGCCTTGGTTCTGCCAGAATGCTGC 325

RESULT 7 E00702 1324 bp RNA linear PAT 29-SEP-1997

LOCUS E00702 CDNA encoding human tumor necrosis factor.

DEFINITION E00702

ACCESSION E00702 GI:2168979

VERSION E00702 JP 1986040221-A/1.

KEYWORDS SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Human.

REFERENCE 1 (bases 1 to 1324)

AUTHORS Baraa, B.A., Debitusudo, B.G., San, H.R. and Guren, E.N.

TITLE TUMOR NECROTIC FACTOR

JOURNAL Patent: JP 1986040221-A 1 26-FEB-1986;

COMMENT OS homosapiens

PN JP 1986040221-A/1

PD 26-FEB-1986

PP 05-JUL-1985 JP 1985149075

PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR 05-JUL-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR 03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454 PI BARAA BUSHIYAN AGAWARU, DEBITSUDO BANNOOMAN GETSUDERU, PI SAN HII RII, PI GUREN EBAN NEDOUIN

PC A61K35/12, A61K35/02, A61K35/14, A61K35/74, A61K37/04, C07H21/02, C07H21/04, PC C12N15/00;

PC strandedness: Single;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

CC *source: cell-type= promyelocytes;

CC *source: cell-line= HL-60;

CC *source: clone= lambda42-4, lambda16-4;

FH Key Location/Qualifiers

FH FT sig_peptide <1. .61

FT mat_peptide 62. .532

FT /product='tumor necrosis factor' FT CDS

FT <1. .535 /product='tumor necrosis factor' FT 3' UTR

FEATURES FT 536. .>1324.

SOURCE Location/Qualifiers 1. .1324

/organism="Homo sapiens"

/mol_type="genomic RNA"

/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG 60
Db 693 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG 752

Qy 61 GAATCTGGAGACCAGGGAGCCTTGGTTCTGCCAGAATGCTGC 104
Db 753 GAATCTGGAGACCAGGGAGCCTTGGTTCTGCCAGAATGCTGC 796

RESULT 6 E0168214 1323 bp DNA linear PAT 02-DEC-1994

LOCUS E0168214

DEFINITION I07953 Sequence 6 from Patent EP 0168214.

ACCESSION I07953 GI:589335

VERSION I07953.1

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1323)

AUTHORS Aggarwal, B.B., Lee, S.H., Goeddel, D.V. and Nedwin, G.E.

TITLE Tumor necrosis factor, methods for its preparation, compositions containing it, DNA encoding it and assay method using such DNA

JOURNAL Patent: EP 0168214-A2 6 15-JAN-1986;

FEATURES Location/Qualifiers 1. .1323

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-24;

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Db 751 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG 810

Qy 61 GAATCTGGAGACCAGGGAGCCTTGGTTCTGCCAGAATGCTGC 854
Db 811 GAATCTGGAGACCAGGGAGCCTTGGTTCTGCCAGAATGCTGC 854

RESULT 8
 LOCUS 103610 1324 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 2 from Patent US 4650674.
 ACCESSION 103610
 VERSION 103610.1 GI:268632
 KEYWORDS Unknown.
 SOURCE Unclassified.
 ORGANISM Aggarwal,B.B. and Lee,S.He.
 FEATURES source
 REFERENCE AUTHORS Synergistic cytotoxic composition
 TITLE Patent: US 4650674-A 2 17-MAR-1987;
 JOURNAL Genentech, Inc.; So. San Francisco, CA
 Location/Qualifiers
 1. .11324 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Query Match Score 104; DB 6; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 1.3e-24;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTCAAACCTGGGCCCTCCAGAACCTCACTGGGCCCTACAGCTTGTGACATCTG 60
 Db 751 GAATTCAAACCTGGGCCCTCCAGAACCTCACTGGGCCCTACAGCTTGTGACATCTG 810
 Qy 61 GAATCTGGAGACCAGGGAGCCAGGCTTGTGGCCAGAATGCTGC 104
 Db 811 GAATCTGGAGACCAGGGAGCCAGGCTTGTGGCCAGAATGCTGC 854
 RESULT 9
 LOCUS 104244 1465 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 2 from Patent US 4677197.
 ACCESSION 104244
 VERSION 104244.1 GI:268725
 KEYWORDS Unknown.
 SOURCE Unclassified.
 ORGANISM Lin,L.S. and Yamamoto,R.
 FEATURES source
 REFERENCE AUTHORS Purification method for tumor necrosis factor
 TITLE Patent: US 4671197-A 2 30-JUN-1987;
 JOURNAL Cetus Corporation; Emeryville, CA
 Location/Qualifiers
 1. .1465 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Query Match Score 104; DB 6; Length 1465;
 Best Local Similarity 100.0%; Pred. No. 1.3e-24;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTCAAACCTGGGCCCTCCAGAACCTCACTGGGCCCTACAGCTTGTGACATCTG 60
 Db 883 GAATTCAAACCTGGGCCCTCCAGAACCTCACTGGGCCCTACAGCTTGTGACATCTG 942
 Qy 61 GAATCTGGAGACCAGGGAGCCAGGCTTGTGGCCAGAATGCTGC 104
 Db 943 GAATCTGGAGACCAGGGAGCCCTTGTTGTGGCCAGAATGCTGC 986
 RESULT 10
 LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 12 from Patent WO9404196.
 ACCESSION A37272.1 GI:2294369
 VERSION A37272.1 GI:2294369
 KEYWORDS unidentified
 SOURCE ORGANISM unidentified
 REFERENCE 1 (bases 1 to 1585)
 AUTHORS Vile,R.G. and Hart,I.R.
 TITLE TUMOUR THERAPY
 JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
 IMP CANCER RES TECH (GB)
 FEATURES Location/Qualifiers
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 Db 1003 GAATTCAAACCTGGGCCCTCCAGAACCTCACTGGGCCCTACAGCTTGTGACATCTG 1062
 Qy 61 GAATCTGGAGACCAGGGAGCCCTTGTTCTGGCCAGAATGCTGC 104
 Db 1063 GAATCTGGAGACCAGGGAGCCCTTGTTCTGGCCAGAATGCTGC 1106
 RESULT 11
 LOCUS 104169 1585 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 1 from Patent US 4677063.
 ACCESSION 104169
 VERSION 104169.1 GI:268716
 KEYWORDS Unknown.
 SOURCE ORGANISM Unclassified.
 REFERENCE AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van Arsdell,J.
 TITLE Human tumor necrosis factor
 JOURNAL Patent: US 4677063-A 1 30-JUN-1987;
 Cetus Corporation; Emeryville, CA
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
 ORIGIN
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 Db 1003 GAATTCAAACCTGGGCCCTCCAGAACCTCACTGGGCCCTACAGCTTGTGACATCTG 1062
 Qy 61 GAATCTGGAGACCAGGGAGCCCTTGTTCTGGCCAGAATGCTGC 104
 Db 1063 GAATCTGGAGACCAGGGAGCCCTTGTTCTGGCCAGAATGCTGC 1106
 RESULT 12
 LOCUS 104198 1585 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 1 from Patent US 4677064.
 ACCESSION 104198
 VERSION 104198.1 GI:268719

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: September 2, 2005, 18:45:43 ; Search time 319.075 Seconds
(without alignments)
1929.494 Million cell updates/sec

08-801-3712-1

gapgap 18⁻⁸ Gapext 1-8

90205 8878 2969870667 20543100

Mathematics 2018, 6, 108

d
C
P
4
M
T
T

Maximum Match 1883

genebeem 9806

Genealogical Data for the First Families of America

geneseqn2001as : *

`geneseq2002as::*`

genesetcm2003aa

卷之三

geuseseqn2003as : *

- geneseqm2004bs :: *

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

Result No.	Score	Query	Match Length	DB ID	Description
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2	104	100.0	787	2	Aaz20979 Human TNF
3	104	100.0	792	13	Adr12297 Human tum
4	104	100.0	1275	1	Aan60558 Sequence
5	104	100.0	1323	1	Aan60363 Sequence
6	104	100.0	1324	3	Aaa34963 Human ade
7	104	100.0	1324	3	Aaf21085 Human low
8	104	100.0	1324	10	Abz96779 Human nuc
9	104	100.0	1324	11	Abd20628 Human pul
10	104	100.0	1560	1	Aan80219 Sequence
11	104	100.0	1581	12	Adq83817 Human tum
12	104	100.0	1585	1	Aan60557 Sequence
13	104	100.0	1585	8	Aca64836 Human TNF
14	104	100.0	1585	10	Adf76346 Novel hum
15	104	100.0	1585	11	Adi32003 Human cDN
16	104	100.0	1585	12	Ado19587 Human PRC
17	104	100.0	1585	13	Adr24640 Breast can
18	104	100.0	1585	13	Adp54654 Human PRC
19	104	100.0	1606	1	Aan60446 Sequence
20	104	100.0	1606	2	Aat15424 Human tum

Result No.	Score	Query	Match	Length	DB ID	Description
1	104	100.0	104	3	Aaz99816	Cis-actin
2	104	100.0	787	2	AAZ20979	Human TNF
3	104	100.0	792	13	ADR12297	Human tu
4	104	100.0	1275	1	AAN60558	Sequence
5	104	100.0	1323	1	AAN60363	Sequence
6	104	100.0	1324	3	Aaa34963	Human ade
7	104	100.0	1324	3	AAF21085	Human low
8	104	100.0	1324	10	ABZ96779	Abz96779 Human nu
9	104	100.0	1324	11	ABD20628	Human pu
10	104	100.0	1560	1	AANB0219	Sequence
11	104	100.0	1581	12	ADQ83817	Adq83817 Human tu
12	104	100.0	1585	1	AAN60557	Sequence
13	104	100.0	1585	8	ACA64836	Aca64836 Human TNF
14	104	100.0	1585	10	ADF76346	Adf76346 Novel hu
15	104	100.0	1585	11	ADI32003	Human cD
16	104	100.0	1585	12	ADO19587	Human PR
17	104	100.0	1585	13	ADR24640	Adr24640 Breast c
18	104	100.0	1585	13	ADP54654	Adp54654 Human PR
19	104	100.0	1606	1	AAN60446	Sequence
20	104	100.0	1606	2	AAT15424	Aat15424 Human tum

Regulation of gene expression by mRNA splicing is carried out using a cis-acting nucleotide sequence controlled by phosphorylation of the alpha-subunit of eukaryotic initiation factor 2.

ALIGNMENTS

RESULT 1
AAZ99816
ID AAZ99816 standard; RNA; 104 BP.
XX
AC AAZ99816;
XX
DT 12-JUL-2000 (first entry)
XX
DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX
KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy;
KW

Homo sapiens.

WO2000014255-A1.

16-MAR-2000.

06-SEP-1999; 99WO-IL000483.

07-SEP-1998; 98IL-00126112.

26-OCT-1998; 98IL-00126757.

(YISS) YISSUM RES & DEV CO.

Kaempfer R, Osman F, Jarrous N, Ben-Aouli Y;

WPI; 2000-257000/22.

Regulation of gene expression by mRNA splicing is carried out using a cis-acting nucleotide sequence controlled by phosphorylation of the alpha-subunit of eukaryotic initiation factor 2.

Claim 4; Page 15; 75pp; English.

The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic

initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslatable region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the invention.

XX SQ sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 3; Length 104;
 Best Local Similarity 100.0%; Pred. No. 3.1e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCCTGACATCTG 60
 Db 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCCTGACATCTG 60
 Qy 61 GAATCTGGAGACCAGGGAGCCCTTTGGGTTCTGGCCAGAAATGGCTGC 104
 Db 61 GAATCTGGAGACCAGGGAGCCCTTTGGGTTCTGGCCAGAAATGGCTGC 104
 RESULT 2
 AAZZ20979 ID AAZZ20979 standard; DNA; 787 BP.
 XX AC AAZZ20979;
 XX DT 30-NOV-1999 (first entry)
 XX DE Human TNFalpha 3'UTR.
 XX KW tumour necrosis factor alpha; apoptosis; inflammation;
 XX KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
 XX KW psoriasis; graft versus host disease; lupus erythematosus; diabetes;
 XX KW ankylosing spondylitis; rheumatoid arthritis; dsB.
 XX OS Homo sapiens.
 XX PN WO9943840-A1.
 XX PD 02-SEP-1999.
 XX PF 12-JAN-1999; 99WO-US000637.
 XX PR 27-FEB-1998; 98US-0076316P.
 XX PA (BOEHLER) BOEHRINGER INGELHEIM PHARM INC.
 XX PI Tatake RJ, Marlin SD, Barton RW;
 XX DR WPI; 1999-527630/44.
 XX PT A chimeric polynucleotide consisting of a tissue necrosis factor (TNF) promoter and an apoptosis-inducing Granzyme B polynucleotide.
 XX PS Example 1; Page 60-61; 71pp; English.

CC undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide CC may be useful for treating inflammatory disorders such as multiple CC sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus CC host disease, lupus erythematosus, insulin-dependent (type I) diabetes CC mellitus, ankylosing spondylitis, and in particular, rheumatoid CC arthritis. The use of such chimeric nucleotides offers simpler and CC cheaper long-term relief, in comparison with existing conventional CC pharmaceutical and invasive surgery methods CC
 XX SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 2; Length 787;
 Best Local Similarity 100.0%; Pred. No. 5.4e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCCTGACATCTG 60
 Db 222 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCCTGACATCTG 281
 Qy 61 GAATCTGGAGACCAGGGAGCCCTTTGGGTTCTGGCCAGAAATGGCTGC 104
 Db 282 GAATCTGGAGACCAGGGAGCCCTTTGGGTTCTGGCCAGAAATGGCTGC 325
 RESULT 3
 ADR12297 ID ADR12297 standard; DNA; 792 BP.
 XX AC ADR12297;
 XX DT 21-OCT-2004 (first entry)
 XX DE Human tumour necrosis factor alpha 3'-untranslated region DNA.
 XX KW ss; cytosstatic; VEGF modulator; angiogenesis inhibitor;
 XX UTR-dependent expression; vascular endothelial growth factor;
 XX untranslated region; cancer; angiogenesis.
 XX Homo sapiens.
 XX OS Homo sapiens.
 XX PN WO2004065561-A2.
 XX PD 05-AUG-2004.
 XX PF 21-JAN-2004; 2004WO-US001643.
 XX PR 21-JAN-2003; 2003US-0441637P.
 XX PA (PTCT-) PTC THERAPEUTICS INC.
 XX PI Cao L, Trifillis P;
 XX DR WPI; 2004-571681/55.
 XX PT Identifying modulators of untranslated region-dependent expression of a PT VEGF gene, useful for treating cancer, comprises contacting a compound PT with a cell or translation mixture containing a reporter gene linked to a PT VEGF gene UTR.
 XX PS Example; SEQ ID NO 6; 251pp; English.
 CC A method of identifying (M1) a compound that modulates untranslated CC region-dependent expression of a vascular endothelial growth factor CC (VEGF) gene comprising contacting a member of a library of compounds with CC a cell or cell-free translation mixture containing a reporter gene CC operably linked to an untranslated region (UTR) of the VEGF gene, and CC detecting expression of the reporter gene. A compound is identified as CC modulator of the reporter gene. A compound is identified as CC modulator of the reporter gene in the presence CC of the compound is altered as compared to that in the absence of the CC compound or in the presence of a control. Compounds identified by M1 are CC useful for treating, preventing or ameliorating cancer or its symptoms, CC and/or for inhibiting angiogenesis. This sequence corresponds to a CC therapeutic untranslated region used in the invention.

CC transmitters, defensins, growth factors, vasoactive peptides and CC receptors, binding proteins and malignancy associated proteins. The CC antisense oligonucleotides may be used in this way to treat disorders CC including respiratory obstruction (especially pulmonary obstruction CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or CC surfactant hypoproduction which are associated with a disease or CC condition selected from pulmonary vasoconstriction, inflammation, CC allergies, asthma, impeded respiration, respiratory distress syndrome CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD), CC pulmonary transplantation rejection, pulmonary infections, bronchitis, CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide CC fragments and antisense oligonucleotides used in the exemplification of CC the present invention

XX Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 104; DB 3; Length 1324;

Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACAGCTTGTGATCCCTGACATCTG 60
Db 751 GAATTCAAACCTGGGCCTCCAGAACTCACAGCTTGTGATCCCTGACATCTG 810

Qy 61 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104
Db 811 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 854

RESULT 8
ABZ96779 ID ABZ96779 standard; DNA; 1324 BP.

XX AC ABZ96779;
XX DT 17-OCT-2003 (First entry)
XX DE Human nucleic acid sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiallergic;
KW immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
OS Homo sapiens.
PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 12021; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
PT nucleic acids associated with lung airway or lung dysfunction, and
PT

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

XX SQ Query Match 100.0%; Score 104; DB 10; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACAGCTTGTGATCCCTGACATCTG 60
Db 751 GAATTCAAACCTGGGCCTCCAGAACTCACAGCTTGTGATCCCTGACATCTG 810

Qy 61 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104
Db 811 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 854

RESULT 9
ABD20628 ID ABD20628 standard; DNA; 1324 BP.
XX AC ABD20628;
XX DT 29-JUL-2004 (First entry)
Human pulmonary and inflammatory target DNA #239.
XX DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX PD 31-OCT-2002.
XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX PR 23-APR-2002; 2002WO-US013143.
XX PR 24-APR-2001; 2001US-0286036P.

XX DR WPI; 2003-093058/08.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PR 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX DR WPI; 2003-093058/08.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PR 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX DR WPI; 2003-093058/08.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PR 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX DR WPI; 2003-093058/08.

PT bronchodilating agent.
 XX
 PS Claim 15; SEQ ID NO 12021; 763pp; English.
 XX This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immuno suppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it.

SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 11; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 6.2e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 751 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 60
 Qy 1 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 60
 Db 811 GAATCTGGAGACCAGGGAGCCCTACAGCTTGTGATCCCTGACATCTG 810
 Qy 61 GAATCTGGAGACCAGGGAGCCCTACAGCTTGTGATCCCTGACATCTG 104
 Db 811 GAATCTGGAGACCAGGGAGCCCTACAGCTTGTGATCCCTGACATCTG 854

RESULT 10
 AAN80219 ID AAN80219 standard; DNA; 1560 BP.
 XX AC AAN80219;
 DT 28-DEC-1990 (first entry)
 DE sequence of pE4 encoding human tumour necrosis factor (TNF).
 KW Lymphokine; antitumour; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 86. .313
 FT /*tag= a
 FT mat_peptide 314. .787
 FT /*tag= b
 XX
 PN WO8806625-A.
 XX
 PD 07-SEP-1988.
 PR 18-OCT-2002; 2002US-0418988P.
 XX PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX PI Wu TD, Zhou Y;
 DR WPI; 2004-534300/51.

XX
 PT 25-JAN-1988; 88WO-US000183.
 XX
 PR 26-FEB-1987; 87US-00019221.
 XX PA (CETU) CETUS CORP.
 XX PI Mark DF, Lin LS, Thomson JW, Yamamoto R;
 XX WPI; 1988-271165/38.
 DR P-PSDB; AAP80728.
 XX Human tumour necrosis factor mutants - having comparable biological activity with improved stability and ease of purification.
 XX PS Disclosure; Fig 1-1 to 1-2; 51pp; English.
 XX A human TNF protein which is modified from the sequence shown in AAP80728, including naturally occurring allelic variants is claimed. Also claimed are: recombinant DNA sequences encoding the protein (AAN80219) and control sequences for expression; a vector; a transformed host cell; a method of producing the protein by culturing the host cell; pharmaceutical compsn. of the protein and a method of treating tumour burden with the compsn. The mutants are capable of the range of biological activities exhibited by native TNF but exhibit improved stability and ease of purification.
 XX SQ Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 1; Length 1560;
 Best Local Similarity 100.0%; Pred. No. 6.5e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 60
 Db 1003 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 1062
 Qy 61 GAATCTGGAGACCAGGGAGCCCTACAGCTTGTGATCCCTGACATCTG 104
 Db 1063 GAATCTGGAGACCAGGGAGCCCTACAGCTTGTGATCCCTGACATCTG 1106
 Qy 1 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 60
 ID ADQ83817 Standard; cDNA; 1581 BP.
 AC ADQ83817;
 XX DT 07-OCT-2004 (First entry)
 XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #631.
 XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
 XX KW cancer; cell proliferative disorder; gene; ss.
 XX OS Homo sapiens.
 XX PN WO2004060270-A2.
 XX PD 22-JUL-2004.
 XX PF 15-OCT-2003; 2003WO-US029126.
 XX PR 18-OCT-2002; 2002US-0418988P.
 XX PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX PI Wu TD, Zhou Y;
 DR WPI; 2004-534300/51.

New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.

XX
PPT
PPT
PS Claim 1; SEQ ID NO 631; 5504pp; English.

The present invention describes an isolated tumour-associated antigen target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container the composition of matter contained within the container; (12) methoh inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of cell proliferative disorder or cancer. The present sequence represents human TAT cDNA sequence from the present invention.

Key Location/Qualifiers
FT 86. .313
FT /*tag= a
FT mat_peptide 314. .787
FT /*tag= b
XX
PN WO8604606-A.
XX
PD 14-AUG-1986.
XX
PF 03-FEB-1986; 86WO-US0000236.
XX
PR 07-FEB-1985; 85US-00698939.
XX
PA (CETUS) CETUS CORP.
XX
PI Mark DF, Lin LS, Lu SDY, Wang AM,
XX
WPI; 1986-225458/34.
DR P-PSDB; AAP60655.
XX
PT New synthetic muteins of human tumour
PT by direct mutagenesis and retain ant
XX
PS Disclosure; Fig 1; 47pp; English.
XX
CC The sequence encoding TNF produced by
CC line (HL-60, ATCC no.CCL240) has been
CC AAN60557). Neither of the cysteine in
CC sequence appears to be involved in claim
CC a novel synthetic mutein of a having at least one cysteine residue
CC essential to the activity and having residues deleted or replaced by another
CC claimed
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389
Query Match 100.0%; Score
Best Local Similarity 100.0%; Pred.
Matches 104; **Conservative** 0; **Mism**
Qy 1 GAATTCAAACCTGGGCCTCCAGAACTC
Db 1003 GAATTCAAACCTGGGCCTCCAGAACTC
Qy 61 GAATCTGGAGACCAGGGAGCCTTGGT
Db 1063 GAATCTGGAGACCAGGGAGCCTTGGT

RESULT 13
ID ACA64836 standard; DNA; 1585 BP.
XX
AC ACA64836;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human TNF-alpha DNA corresponding to
KW Human; chronic inflammatory joint disease
KW antiinflammatory; cytostatic; antiarthritis
KW immunosuppressive; gene therapy; etiopathogenesis
XX
OS Homo sapiens.
XX
PN DE10127572-A1.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2001; 2001DE-01027572.
XX

XX PR 09-FEB-1998; 98US-00023655.
 XX PA (INCY-) INCYTE CORP.
 XX PI Cocks BG, Stuart SG, Seilhamer JJ;
 XX DR WPI; 2003-895307/82.

PT A composition comprising a plurality of cDNAs, useful for detecting
 PT altered expression of genes in an immunological response or for
 PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
 PT or osteoarthritis.

XX PS Claim 1; SEQ ID NO 1329; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs
 CC for detecting the altered expression of genes in an immunological
 CC response. The invention also relates to a method of diagnosing or
 CC monitoring the treatment of an immunopathological condition in a sample,
 CC comprising obtaining nucleic acids from a sample, contacting the nucleic
 CC acids of the sample with an array comprising the plurality of cDNAs under
 CC conditions to form one or more hybridisation complexes, detecting the
 CC hybridisation complexes and comparing the levels of the detected
 CC hybridisation complexes with the level of hybridisation complexes
 CC detected in a non-diseased sample, where an altered level of the detected
 CC hybridisation complexes correlates with the presence of an
 CC immunopathological condition. Also disclosed are an expression profile
 CC comprising a microarray and a plurality of detectable complexes and a
 CC method for identifying a plurality of polynucleotide probes. The cDNAs
 CC are useful as hybridisable array elements in a microarray for monitoring
 CC the expression of target polynucleotides. The microarray can be used in
 CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
 CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
 CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
 CC identifying agents for the treatment of the diseases. The microarray may
 CC also be used in drug discovery and development, toxicological and
 CC carcinogenicity studies, forensics or pharmacogenomics. The composition
 CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
 CC genomic fragments. This sequence represents a human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	11	1585
Matches	104;	Pred. No.	6.5e-25;
	Conservative	Mismatches	0;
		Indels	0;
		Gaps	0;
Qy	1	GAATTCAA	ACTGGGCCCTCAGAACTCACTGGGCCCTACAGCTTGTACATCTG 60
Db	1003	GAATTCAA	ACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGTACATCTG 1062
Qy	61	GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 104	
Db	1063	GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 1106	

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 Job time : 326.075 secs

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NCM nucleic - nucleic search, using sw model
Run on: September 2, 2005, 23:36:03 ; Search time 2377.85 Seconds
(without alignments)
1664.816 Million cell updates/sec

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scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters:	68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
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3:: gb_ncc; *
4:: gb_est3; *
5:: gb_est4; *
6:: gb_est5; *
7:: gb_est6; *
8:: gb_gss1; *

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	104	100.0	474	5	BX118951	BX118951		
2	104	100.0	630	6	CB528492	CB528492	UI-H-FT2-	
3	104	100.0	645	6	CD370363	CD370363	UI-H-FT1-	
4	104	100.0	688	6	CD367676	CD367676	UI-H-FT1-	
5	104	100.0	696	6	CA307225	CA307225	UI-H-FT1-	
6	104	100.0	699	6	CD364761	CD364761	UI-H-FT2-	
7	104	100.0	703	6	CD368142	CD368142	UI-H-FT1-	
8	104	100.0	713	6	CA308256	CA308256	UI-H-FT1-	
9	104	100.0	719	6	CB528694	CB528694	UI-H-FT2-	
10	104	100.0	722	5	BQ007008	BQ007008	UI-H-EI1-	
11	104	100.0	722	6	CA307062	CA307062	UI-H-FT1-	
12	104	100.0	722	6	CD364988	CD364988	UI-H-FT2-	
13	104	100.0	723	6	CA308777	CA308777	UI-H-FT1-	
14	104	100.0	723	6	CD368116	CD368116	UI-H-FT1-	
15	104	100.0	724	6	CA309711	CA309711	UI-H-FT1-	
16	104	100.0	726	6	CA310368	CA310368	UI-H-FT1-	
17	104	100.0	726	6	CD368929	CD368929	UI-H-FT1-	
18	104	100.0	742	6	CA309509	CA309509	UI-H-FT1-	
19	104	100.0	744	6	CD366187	CD366187	UI-H-FT1-	
20	104	100.0	748	6	CA306559	CA306559	UI-H-FT1-	
21	104	100.0	1068	1	AL543083	AL543083	AL543083	
22	103	99.0	248	7	T29839	T29839	EST97164	Hu
23	103	99.0	693	6	CD367625	CD367625	UI-H-FT1-	
24	102	98.5	693	6	CD367429	CD367429	UI-H-FT1-	

ALIGNMENTS

RESULT	1					
BX118951						
LOCUS	BX118951	474 bp	mRNA	linear	EST 10-FEB-2003	
DEFINITION	BX118951 Soares fetal heart NBHH19W Homo sapiens cDNA clone					
IMAGP998L124300 ; IMAGE:1693595, mRNA sequence.						
ACCESSION	BX118951					
VERSION	BX118951.1	GI:27882696				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)	:				
ORGANISM	Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 474)					
AUTHORS	Ebert, L., Heil, O., Hennig, S., Neubert, P., Radelof, U., Schneider, D. and Korn, B.					
TITLE	Human Unigeneset - RZPD3					
JOURNAL	Unpublished (2003)					

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998L124300.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No. 972)
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGAACAGCTATGAC.

FEATURES

source

Location/Qualifiers

1. .474

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP998L124300 ; IMAGE:1693595"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oTGo(dT) primer (synthetic)

double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a $Cot = 5$. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

ORIGIN

Query	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60
	65	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCCTACAGCTTGATCCCCGACATCTG	124
Db	125	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	168

RESULT 2

LOCUS	CB528492	CB528492	630 bp	mRNA	linear	EST 05-AUG-2004
DEFINITION	UI-H-FT2-bjd-e-20-0-UI.81	NCI CGAP_FT2	Homo sapiens	CDNA clone		
AUTHORS	UI-H-FT2-bjd-e-20-0-UI	3'	mRNA sequence.			
ACCESSION	CB528492					
VERSION	CB528492.1	GI:29388228				
KEYWORDS	EST.					

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 630) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA Sequence: 1-29, >AT rich#Low complexity (matched compliment)

205-279, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

Source

1.	630	Location/Qualifiers
		/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/clone="UI-H-FT2-bjd-e-20-0-UI"
		/tissue_type="Alveolar Macrophage"
		/dev_stage="Adult"
		/lab_host="DH10B (Life Technologies)"
		/lab_host="NCI CGAP FT1"

/note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a

modified polylinker; Site_1: Ecor I; Site_2: Not I;

NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of

the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library conditions).

construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT2

TAG_SEQ=GCCATATGCCG

ORIGIN

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	125	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	168	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	125	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	168	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	60	630
Db	503	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGATCCCCGACATCTG	444	
Qy	61	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	104	
Db	443	GAATCTGGAGACCAGGGAGCCCTACAGCTGGGCCAGAATGCTGC	400	

Query	Match	Score	DB	Length
Qy	1	GAATTCAAACCTGG		

NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT1

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	100.0%	Score	104	DB	6	Length	645
Best Local Similarity	100.0%	Pred. No.	2.8e-21				
Matches	104	Conservative	0	Mismatches	0	Gaps	0

Qy 1 GAATTCAA~~ACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCC~~TGACATCTG 60
 Db 592 GAATTCAA~~ACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCC~~TGACATCTG 533

Qy 61 GAATCTGGAGACCAGGAGCCTTGGTTCTGCCAGAA~~TGTGC~~ 104
 Db 532 GAATCTGGAGACCAGGAGCCTTGGTTCTGCCAGAA~~TGTGC~~ 489

RESULT 4

CD367676/c

LOCUS CD367676 688 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-FT1-bjr-1-14-0-UI-S1 NCI CGAP_FT1 Homo sapiens cDNA clone
 UI-H-FT1-bjr-1-14-0-UI 3', mRNA sequence.

ACCESSION CD367676

VERSION CD367676.1 GI:31151766

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/nicgap.

AUTHORS

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 The following repetitive elements were found in this cDNA

ORIGIN

Query Match	100.0%	Score	104	DB	6	Length	688
Best Local Similarity	100.0%	Pred. No.	2.8e-21				
Matches	104	Conservative	0	Mismatches	0	Gaps	0

Qy 1 GAATTCAA~~ACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCC~~TGACATCTG 60
 Db 367 GAATTCAA~~ACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCC~~TGACATCTG 308

Qy 61 GAATCTGGAGACCAGGAGCCTTGGTTCTGCCAGAA~~TGTGC~~ 104
 Db 307 GAATCTGGAGACCAGGAGCCTTGGTTCTGCCAGAA~~TGTGC~~ 264

RESULT 5

CA307225/c

LOCUS CA307225
 DEFINITION UI-H-FT1-bhu-n-04-0-UI-S1 NCI CGAP_FT1 Homo sapiens cDNA clone
 UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.

ACCESSION CA307225
 VERSION CA307225.1 GI:24470279
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 696) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	Db 534	GAATCTGGAGACCGAGCCTTGGTTCTGCCAGAATGCTGC 491
AUTHORS TITLE JOURNAL COMMENT		RESULT 6 CD364761/c
Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Dr. Gary W. Hunninghake, U of I CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu The following repetitive elements were found in this cDNA Sequence: 296-370, >(TAAA)n#Simple_repeat Seq primer: M13 FORWARD POLYA=Yes.	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 699) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	699 bp mRNA linear EST 05-AUG-2004 UI-H-FT2-bjm-j-11-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence. CD364761 CD364761.1 GI:31148851 EST.
FEATURES source	Location/Qualifiers 1. . 696 /organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon:9606" /clone="UI-H-FT1-bhu-n-04-0-UI" /tissue_type="Alveolar Macrophage" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI CGAP FT1" /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT1 TAG_SEQ=GGCCATGCCG"	FEATURES source /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP FT1 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT2 TAG_SEQ=GGCCATGCCG"
ORIGIN	Query Match Score 104; DB 6; Length 696; Best Local Similarity 100.0%; Pred. No. 2.8e-21; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%; Score 104; DB 6; Length 696; Best Local Similarity 100.0%; Pred. No. 2.8e-21; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GAATTCAAACGTGGCCCTCCGAACACTGGGCCCTACAGCTTGTACATCTG 60 594 GAATTCAAACGTGGCCCTCCGAACACTGGGCCCTACAGCTTGTACATCTG 535	Query Match Score 104; DB 6; Length 699;
Db		
Qy	61 GAATCTGGAGACCAAGGAGCCAGCTTGGTTCTGCCAGAAATGCTGC 104	

Best Local Similarity 100.0%; Pred. No. 2.9e-21; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 594 GAATTCAAACGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 535

Qy 61 GAATCTGGAGACCAGGGAGCCCTTGTTCTGGGCCAGAATGCTGC 104
Db 534 GAATCTGGAGACCAGGGAGCCCTTGTTCTGGGCCAGAATGCTGC 491

RESULT 7
LOCUS CD368142/c 703 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bjv-e-20-0-UI.81 NCI CGAP FT1 Homo sapiens cDNA clone
VERSION CD368142.1 GI:311522322
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 298-372, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES source

Location/Qualifiers

1. .703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-e-20-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 537

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTGTGACATCTG 60
Db 596 GAATTCAAACACTGGGGCTCCAGAACTCACT

(some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT1

TAG_SEQ=GGCCATGCCG

ORIGIN

Query Match	Score	DB	Length
Best Local Similarity	100.0%	6	713;
Matches 104;	Conservative	2.9e-21;	
Mismatches 0;	Indels 0;	Gaps 0;	

Qy 1 GAATTCAA~~ACTGGGGCTCCAGAACTCA~~TGGGCC~~TACAGCTTGATCCC~~TGACATCTG 60
Db 594 GAATTCAA~~ACTGGGGCTCCAGAACTCA~~TGGGCC~~TACAGCTTGATCCC~~TGACATCTG 535

Qy 61 GAATCTGGAGACCAGGAGCTTGGTTCTGGCCAGAA~~TGCTGC~~ 104
Db 534 GAATCTGGAGACCAGGAGCTTGGTTCTGGCCAGAA~~TGCTGC~~ 491

RESULT 9
LOCUS CB528694
DEFINITION UI-H-FT2-bjd-1-22-0-UI-S1 NCI CGAP_FT2 Homo sapiens CDNA clone
ACCESSION CB528694
VERSION CB528694.1 GI:29388630
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this CDNA
Sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .719

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FT2-bjd-1-22-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_FT2"

/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site 1: ECO RI; Site 2: Not I;"

NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples

were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of

the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24

hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus

moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;

wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 24 hours.

The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT2

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	Score	DB	Length
Best Local Similarity	100.0%	6	719;
Matches 104;	Conservative	2.9e-21;	
Mismatches 0;	Indels 0;	Gaps 0;	

Qy 1 GAATTCAA~~ACTGGGGCTCCAGAACTCA~~TGGGCC~~TACAGCTTGATCCC~~TGACATCTG 60
Db 594 GAATTCAA~~ACTGGGGCTCCAGAACTCA~~TGGGCC~~TACAGCTTGATCCC~~TGACATCTG 535

Qy 61 GAATCTGGAGACCAGGAGCTTGGTTCTGGCCAGAA~~TGCTGC~~ 104
Db 534 GAATCTGGAGACCAGGAGCTTGGTTCTGGCCAGAA~~TGCTGC~~ 491

RESULT 10
LOCUS BQ007008/c
DEFINITION UI-H-EII-azb-j-22-0-UI-S1 NCI CGAP_EII Homo sapiens cDNA clone IMAGE:5846517 3', mRNA sequence.
ACCESSION BQ007008
VERSION BQ007008.1 GI:19731908
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this CDNA
Sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLY A=Yes.

FEATURES Location/Qualifiers
source 1. .719

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjd-1-22-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site 1: ECO RI; Site 2: Not I;"
NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 24 hours.

The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT2

TAG_SEQ=GGCCATGCCG"

Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 The following repetitive elements were found in this CDNA sequence: 297-371, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source
 FEATURES source
 Location/Qualifiers
 1. . 722
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5846517"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP EII"
 /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP EII is a normalized cDNA library containing the following tissue (S): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTGGCAC.
 TAG TISSUE=chondrosarcoma
 TAG_LIB=UI-H-EII
 TAG_SEQ=ACACTGGCAC"

ORIGIN
 Query Match 100.0%; Score 104; DB 5; Length 722;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 104; Conservative 0; Mismatches 0; Gaps 0;

Qy	1	GAATTCAA ACTGGGCCTCCAGAACTC TGGGCTTACAGCTTGTATCTG	60
Db	595	GAATTCAA ACTGGGCCTCCAGAACTC TGGGCTTACAGCTTGTATCTG	536
Qy	61	GAATCTGGAGACCAGGGAGCC TGGTTCTGGCTGCCAGAATGCTGC 104	
Db	535	GAATCTGGAGACCAGGGAGCC TGGTTCTGGCTGCCAGAATGCTGC 492	

RESULT 11
 CA307062/c
 LOCUS CA307062 722 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-FT1-bhu-o-04-0-UI.81 NCI CGAP FT1 Homo sapiens CDNA clone
 UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.
 ACCESSION CA307062
 VERSION CA307062.1 GI:24470116
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. (bases 1 to 722)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 DNA Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this CDNA sequence: 295-369, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source
 FEATURES source
 Location/Qualifiers
 1. . 722
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bhu-o-04-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV EGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT1
 TAG_SEQ=GGCCATGCCG"

ORIGIN
 Query Match 100.0%; Score 104; DB 6; Length 722;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCAA ACTGGGCCTCCAGAACTC TGGTCTGGCTGCCAGAATGCTGC	60
Db	593	GAATTCAA ACTGGGCCTCCAGAACTC TGGTCTGGCTGCCAGAATGCTGC	534
Qy	61	GAATCTGGAGACCAGGGAGCC TGGTTCTGGCTGCCAGAATGCTGC 104	
Db	533	GAATCTGGAGACCAGGGAGCC TGGTTCTGGCTGCCAGAATGCTGC 490	

RESULT 12
 CD364988/c
 LOCUS CD364988
 DEFINITION UI-H-FT2-bjn-c-04-0-UI.81 NCI CGAP FT2 Homo sapiens CDNA clone
 ACCESSION CD364988
 VERSION CD364988.1 GI:31149078
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 722)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
COMMENT
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
Sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .722
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-c-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtracted according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG
Db	595	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG
Qy	61	GAATCTGGAGACCAGGGAGCTTGGTTGGCCAGAATGCTGC
Db	535	GAATCTGGAGACCAGGGAGCTTGGTTGGCCAGAATGCTGC

RESULT 13
CA308777/c

LOCUS CA308777 723 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bhy-b-23-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone.
REFERENCE 1 (bases 1 to 723)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
VERSION CA308777.1 GI:24471831
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Unpublished (1997)
Contact: Robert Straussberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .723
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtracted according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG
Db	595	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG
Qy	61	GAATCTGGAGACCAGGGAGCTTGGTTGGCCAGAATGCTGC
Db	535	GAATCTGGAGACCAGGGAGCTTGGTTGGCCAGAATGCTGC

RESULT 13
CA308777/c

LOCUS CA308777 723 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bhy-b-23-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone.
REFERENCE 1 (bases 1 to 723)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
VERSION CA308777.1 GI:24471831
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Unpublished (1997)
Contact: Robert Straussberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .723
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtracted according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG
Db	595	GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGTACATCTG
Qy	61	GAATCTGGAGACCAGGGAGCTTGGTTGGCCAGAATGCTGC
Db	535	GAATCTGGAGACCAGGGAGCTTGGTTGGCCAGAATGCTGC

RESULT 13
CA308777/c

Query Match 100.0%; Score 104; DB 6; Length 723;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCTCCAGAACTCACTGGGCCAACGCTTACAGCTTGATCCCTGACATCTG 60
 Db 595 GAATTCAAACCTGGGCTCCAGAACTCACTGGGCCAACGCTTACAGCTTGATCCCTGACATCTG 536

Qy 61 GAATCTGGAGACCAGGGAGCCAGGAGCCAGGAGCTTGGTTCTGGCCAGGAATGCTGC 104
 Db 535 GAATCTGGAGACCAGGGAGCCAGGAGCTTGGTTCTGGCCAGGAATGCTGC 492

TAG_LIB=UI-H-FT1
 TAG_SEQ=GGCCATGCCG"

RESULT 14

LOCUS CD368116/c 723 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-FT1-bjv-a-04-0-UI .81 NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-bjv-a-04-0-UI 3', mRNA sequence.

VERSION CD368116
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 723)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsbs-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/gap.html>
 The following repetitive elements were found in this cDNA
 sequence: 297-371, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source

Location/Qualifiers

1. .723
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bjv-a-04-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lennon and Soares, Genome

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 723;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCTCCAGAACTCACTGGGCCAACGCTTACAGCTTGATCCCTGACATCTG 60
 Db 595 GAATTCAAACCTGGGCTCCAGAACTCACTGGGCCAACGCTTACAGCTTGATCCCTGACATCTG 536

RESULT 15

LOCUS CA309711/c 724 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-FT1-bic-b-17-0-UI .81 NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-bic-b-17-0-UI 3', mRNA sequence.

ACCESSION CA309711
 VERSION CA309711.1 GI:24472765
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 724)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsbs-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 297-371, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source

Location/Qualifiers

1. .724
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bic-b-17-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lennon and Soares, Genome

incubations following isolation by bronchoalveolar lavage (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pR7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query	Match	100.0%	Score	104;	DB	6;	Length	724;
	Best Local Similarity	100.0%	Pred. No.	2.9e-21;				
	Matches	104;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GAATTCAA	ACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGTACATCTG	60				
Db	595	GAATTCAA	ACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGTACATCTG	536				
Qy	61	GAATCTGGAGACCAGGGAGCTTGGTTCTGGCCAGAATGCTGC	104					
Db	535	GAATCTGGAGACCAGGGAGCTTGGTTCTGGCCAGAATGCTGC	492					

Search completed: September 3, 2005, 02:11:40
Job time : 2384.85 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 13:14:57 ; Search time 424.49 seconds
 (without alignments)
 400.888 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaaacctgggcctcc.....99ttttggccagaatgtgc 104

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cggn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cggn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cggn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cggn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cggn2_6/ptodata/1/ina/PCFTUS_COMB.seq:*
 6: /cggn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	104	100.0	787	4	US-09-032-297A-13		Sequence 13, Appli
2	104	100.0	787	4	US-09-229-151C-7		Sequence 7, Appli
3	104	100.0	1585	4	US-09-023-655-1329		Sequence 1329, Ap
4	104	100.0	1587	4	US-09-949-016-5156		Sequence 5156, Ap
5	104	100.0	1643	3	US-08-880-342-36		Sequence 36, Appli
6	104	100.0	1643	3	US-09-505-250-4		Sequence 4, Appli
7	104	100.0	2270	4	US-09-229-151C-13		Sequence 13, Appli
8	104	100.0	2570	4	US-09-229-151C-14		Sequence 14, Appli
9	104	100.0	3634	3	US-09-166-186-1		Sequence 1, Appli
10	104	100.0	3634	3	US-09-313-932-1		Sequence 1, Appli
11	104	100.0	3634	3	US-09-109-663-34		Sequence 34, Appli
12	104	100.0	6682	4	US-09-949-016-16898		Sequence 16898, A
C 13	104	100.0	10728	4	US-09-376-774-5		Sequence 5, Appli
C 14	32.6	31.3	2623	4	US-09-976-594-142		Sequence 142, App
C 15	29.2	28.1	601	4	US-09-949-016-182065		Sequence 182065,
C 16	29.2	28.1	31713	4	US-09-949-016-16960		Sequence 16960, A
C 17	29	27.9	7517	4	US-09-949-016-15603		Sequence 15603, A
C 18	28.4	27.3	19601	4	US-09-949-016-15629		Sequence 15629, A
C 19	28	26.9	28720	3	US-09-341-587-7		Sequence 7, Appli
C 20	28	26.9	40905	4	US-09-949-016-16864		Sequence 16864, A
C 21	27.8	26.7	82125	4	US-09-949-016-13517		Sequence 13517, A
C 22	27.8	26.7	82125	4	US-09-949-016-13518		Sequence 13518, A
C 23	27.4	26.3	601	4	US-09-949-016-165185		Sequence 165185,
C 24	27.4	26.3	102304	4	US-09-949-016-12589		Sequence 12589, A
C 25	27.4	26.3	116592	4	US-09-818-512-3		Sequence 3, Appli
C 26	27.4	26.3	124264	4	US-09-949-016-16396		Sequence 16396, A
C 27	27.4	26.2	412	4	US-09-621-976-19072		Sequence 19072, A

RESULT 1
 US-09-032-297A-13
 ; Sequence 13, Application US/09032297A
 ; Patent No. 6525184
 ; GENERAL INFORMATION:
 / ; APPLICANT: Revati J. Tatake, Steven D. Marlin and Randall W. Barton
 / ; NUMBER OF SEQUENCES: 13
 / ; CORRESPONDENCE ADDRESS:
 / ; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
 / ; ADDRESSEE: Boehringer Ingelheim Corporation
 / ; STREET: 900 Ridgebury Road, P.O. Box 368
 / ; CITY: Ridgefield
 / ; STATE: Connecticut
 / ; COUNTRY: United States of America
 / ; ZIP: 06877-0368
 / ; COMPUTER READABLE FORM:
 / ; MEDIUM TYPE: 3.5" 1.44 Mb diskette
 / ; COMPUTER: IBM PC
 / ; OPERATING SYSTEM: MS DOS
 / ; SOFTWARE: WORD PROCESSING
 / ; CURRENT APPLICATION DATA:
 / ; APPLICATION NUMBER: US/09/032,297A
 / ; FILING DATE: 27-Feb-1998
 / ; CLASSIFICATION: <Unknown>
 / ; PRIOR APPLICATION DATA:
 / ; APPLICATION NUMBER: 60/038,266
 / ; FILING DATE: 28-FEB-97
 / ; ATTORNEY/AGENT INFORMATION:
 / ; NAME: Robert P. Raymond
 / ; REGISTRATION NUMBER: 25089
 / ; REFERENCE/DOCKET NUMBER: 9/121PCT
 / ; TELECOMMUNICATION INFORMATION:
 / ; TELEPHONE: 203-791-6183
 / ; INFORMATION FOR SEQ ID NO: 13:
 / ; SEQUENCE CHARACTERISTICS:
 / ; LENGTH: 787
 / ; TYPE: nucleic acid
 / ; STRANDEDNESS: Single
 / ; TOPOLOGY: linear
 / ; MOLECULE TYPE: <Unknown>
 / ; DESCRIPTION: DNA
 / ; FEATURE:
 / ; NAME/KEY: TNFa 3' untranslated region
 / ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 / ; US-09-032-297A-13
 / ; Query Match Score 104; DB 4; Length 787;
 / ; Best Local Similarity 100.0%; Pred. No. 4.2e-27;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0; FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1329;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1585 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9339737
 US-09-023-655-1329

Query Match 100.0%; Score 104; DB 4; Length 1585;
 Best Local Similarity 100.0%; Pred. No. 5.4e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGCTCCAGAACCTACAGCTTGTGACATCTG 60
 Db 1003 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60

Qy 1 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60
 Db 1062 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 1062

Qy 1 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60
 Db 1003 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60

Qy 1 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60
 Db 1063 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 1106

RESULT 4
 US-09-949-016-5156
 Sequence 5156, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 5156
 LENGTH: 1587
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-5156

Query Match 100.0%; Score 104; DB 4; Length 787;
 Best Local Similarity 100.0%; Pred. No. 4.2e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60
 Db 222 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 281

Qy 1 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60
 Db 282 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 325

Query Match 100.0%; Score 104; DB 4; Length 1587;
 Best Local Similarity 100.0%; Pred. No. 5.4e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60
 Db 1005 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 1064

Qy 1 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 60
 Db 1065 GAATTCAAACACTGGGCTCCAGAACACTGGGCTACAGCTTGTGACATCTG 1108

RESULT 3
 US-09-023-655-1329
 Sequence 1329, Application US/09023655
 Patent No. 6607879
 GENERAL INFORMATION:
 APPLICANT: Cocks, Benjamin G.
 APPLICANT: Susan G. Stuart
 APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 TITLE OF INVENTION: EXPRESSION
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655

RESULT 5
 US-08-880-342-36
 ; Sequence 36, Application US/08880342
 ; Patent No. 6218179
 ; GENERAL INFORMATION:
 ; APPLICANT: Webster, Keith A.
 ; Bishopric, Nanette H.
 ; APPLICANT: Murphy, Brian.
 ; APPLICANT: Laderoute, Keith R.
 ; APPLICANT: Green, Christopher J.
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/880,342
 FILING DATE: 23-JUN-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/IB95/00996
 FILING DATE: 13-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/365,486
 FILING DATE: 23-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1643 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: TNF CDNA HSTNFR (EMBL Accession
 INDIVIDUAL ISOLATE: #X01394)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 153...851
 US-08-880-342-36

Query Match 100.0%; Score 104; DB 3; Length 1643;
 Best Local Similarity 100.0%; Pred. No. 5.5e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTTGATCCCTGACATCTG 60
 Db 1070 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTTGATCCCTGACATCTG 1129

Qy 61 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 104
 Db 1130 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 1173

RESULT 6
 US-09-505-250-4
 ; Sequence 4, Application US/09505250A
 ; Patent No. 6329148
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Glenn
 ; Kao, Peter
 ; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
 ; Triptolides and Death Domain Ligands
 ; FILE REFERENCE: SUN-109PRV2
 ; CURRENT APPLICATION NUMBER: US/09/505,250A
 ; CURRENT FILING DATE: 2000-02-15
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 1643
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (153)...(854)
 US-09-505-250-4

Query Match 100.0%; Score 104; DB 3; Length 1643;
 Best Local Similarity 100.0%; Pred. No. 5.5e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTTGATCCCTGACATCTG 60
 Db 1070 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTTGATCCCTGACATCTG 1129

Qy 61 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 104
 Db 1130 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 1173

RESULT 7
 US-09-229-151C-13
 ; Sequence 13, Application US/09229151C
 ; Patent No. 6537784
 ; GENERAL INFORMATION:
 ; APPLICANT: Tatake, Revati J.
 ; Marlin, Steven D.
 ; APPLICANT: Barton, Randall W.
 ; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
 ; FILE REFERENCE: 9/137
 ; CURRENT APPLICATION NUMBER: US/09/229,151C
 ; CURRENT FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: US 60/076,316
 ; PRIOR FILING DATE: 1998-02-27
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 2.0
 ; SEQ ID NO 13
 ; LENGTH: 2270
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; OTHER INFORMATION: chimeric gene : -706TNFPGB3' UTR
 US-09-229-151C-13

Query Match 100.0%; Score 104; DB 4; Length 2270;
 Best Local Similarity 100.0%; Pred. No. 6.1e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTTGATCCCTGACATCTG 60
 Db 1705 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTTGATCCCTGACATCTG 1764

Qy 61 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 104
 Db 1176 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGGCCAGAATGCTGC 11808

RESULT 8
US-09-229-151C-14
; Sequence 14, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/13/7
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 14
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -1005TNFPGB3' UTR
US-09-229-151C-14

Query Match 100.0%; Score 104; DB 4; Length 2570;
Best Local Similarity 100.0%; Pred. No. 6.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTATCCCTGACATCTG 60
Db 2005 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCCTACAGCTTGTATCCCTGACATCTG 2064
Qy 61 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGCCAGAAATGCTGC 104
Db 2065 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGCCAGAAATGCTGC 2108
Qy 61 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGCCAGAAATGCTGC 104
Db 2868 GAATCTGGAGACCAGGGAGCCCTTGGTTCTGCCAGAAATGCTGC 2911

RESULT 9
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)

RESULT 10
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (982..1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589..1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635..1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589..1634)
; FEATURE:
; NAME/KEY: intron

LOCATION: (1635)..(1821)
 FEATURE:
 NAME/KEY: exon
 LOCATION: (1822)..(1869)
 FEATURE:
 NAME/KEY: intron
 LOCATION: (1870)..(2070)
 FEATURE:
 NAME/KEY: exon
 LOCATION: (2171)..(3381)
 PUBLICATION INFORMATION:
 AUTHORS: Nedwin, G.E.
 AUTHORS: Naylor, S.L.
 AUTHORS: Sakaguchi, A.Y.
 AUTHORS: Smith, D.
 AUTHORS: Jarrett-Nedwin, J.
 AUTHORS: Pennica, D.
 AUTHORS: Goeddel, D.V.
 AUTHORS: Gray, P.W.
 TITLE: Human lymphotoxin and tumor necrosis factor genes:
 TITLE: structure, homology and chromosomal localization
 JOURNAL: Nucleic Acids Res.
 VOLUME: 13
 ISSUE: 17
 PAGES: 6361-6373
 DATE: 1985-09-11
 DATABASE ACCESSION NUMBER: X02910 Genbank
 DATABASE ENTRY DATE: 1997-02-17
 US-09-313-932-1

Query Match 100.0%; Score 104; DB 3; Length 3634;
 Best Local Similarity 100.0%; Pred. No. 7.3e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGCTCCAGAACTCACAGCTTGTACATCTG 60
 Db 2808 GAATTCAAACGGGCTCCAGAACTCACAGCTTGTACATCTG 2867

Qy 61 GAATCTGGAGACCAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 104
 Db 2868 GAATCTGGAGACCAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 2911

RESULT 11
 US-09-109-663-34
 Sequence 34, Application US/09109663
 Patent No. 6227981
 GENERAL INFORMATION:
 APPLICANT: Tu, Guang-Chou
 TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
 TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
 FILE REFERENCE: 9855-3U1
 CURRENT APPLICATION NUMBER: US/09/109,663
 CURRENT FILING DATE: 1998-07-03
 EARLIER APPLICATION NUMBER: 60/051,705
 EARLIER FILING DATE: 1997-07-03
 NUMBER OF SEQ ID NOS: 81
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 34
 LENGTH: 3634
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: TNF(alpha) cDNA
 US-09-109-663-34

Query Match 100.0%; Score 104; DB 3; Length 3634;
 Best Local Similarity 100.0%; Pred. No. 7.3e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGCTCCAGAACTCACAGCTTGTACATCTG 60

RESULT 12
 US-09-949-016-16898
 Sequence 16898, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIORITY APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIORITY APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIORITY APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 16898
 LENGTH: 6682
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-16898

Query Match 100.0%; Score 104; DB 4; Length 6682;
 Best Local Similarity 100.0%; Pred. No. 9e-27;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGCTCCAGAACTCACAGCTTGTACATCTG 60
 Db 4099 GAATTCAAACGGGCTCCAGAACTCACAGCTTGTACATCTG 4158

Qy 61 GAATCTGGAGACCAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 104
 Db 4159 GAATCTGGAGACCAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 4202

RESULT 13
 US-09-376-774-5/c
 Sequence 5, Application US/09376774
 Patent No. 6759236
 GENERAL INFORMATION:
 APPLICANT: Fung, Yuen Kai
 APPLICANT: Gomer, Charles
 APPLICANT: T'Ang, Anne
 TITLE OF INVENTION: Methods To Enhance And Confine Expression
 FILE OF INVENTION: Of Genes
 FILE REFERENCE: D6087
 CURRENT APPLICATION NUMBER: US/09/376,774
 CURRENT FILING DATE: 2003-03-21
 PRIORITY APPLICATION NUMBER: 60/096,947
 PRIOR FILING DATE: 1998-08-18
 NUMBER OF SEQ ID NOS: 5
 SEQ ID NO 5
 LENGTH: 10728
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: recombinant vector pDATH-TNF?

US-09-376-774-5

Query Match 100.0%; Score 104; DB 4; Length 10728;
 Best Local Similarity 100.0%; Pred. No. 1.1e-26;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGCTCCAGAACTCACAGCTTGTACATCTG 60

RESULT 14
 US-09-976-594-142/C
 ; Sequence 142, Application US/09976594
 ; Patent No. 6673549
 ; GENERAL INFORMATION:
 ; APPLICANT: Buchbinder, Jenny
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; CURRENT APPLICATION NUMBER: US/09/976,594
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 142
 ; LENGTH: 2623
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 337187.1
 ; NAME/KEY: unsure
 ; LOCATION: 2612
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-09-976-594-142

Query Match 31.3%; Score 32.6; DB 4; Length 2623;
 Best Local Similarity 58.9%; Pred. No. 0.14;
 Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
 Qy 9 ACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGTACCTGGAATCTGG
 Db 359 ACTGGGTGCTGAGGTAGTGAGGGCTGGCTGGCTGGCTGGAGGGGG 300

Query Match 28.1%; Score 29.2; DB 4; Length 601;
 Best Local Similarity 65.2%; Pred. No. 1.4;
 Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 Qy 6 CAAACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGTACCTGGAATC 65
 Db 355 CAGACTGTGCCACGCAGGCTCCCTGGGGCTTCCTACACCTAGATATTGAAAAC 414

Query Match 28.1%; Score 29.2; DB 4; Length 601;
 Best Local Similarity 65.2%; Pred. No. 1.4;
 Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 Qy 6 CAAACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGTACCTGGAATC 65
 Db 355 CAGACTGTGCCACGCAGGCTCCCTGGGGCTTCCTACACCTAGATATTGAAAAC 414

Search completed: September 2, 2005, 18:55:18
 Job time : 428.49 secs

RESULT 15
 US-09-949-016-182065
 ; Sequence 182065, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 182065
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 15:27:57 ; Search time 478.966 Seconds
 (without alignments)
 1421.994 Million cell updates/sec

Title: US-09-801-371A-1
 Perfect score: 104
 Sequence: 1 gaattccaaactggggccccc.....9gttctggccagaatgtgc 104

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	104	100.0	104	9 US-09-801-371A-5	Sequence 5, Appli
3	104	100.0	787	18 US-10-356-308A-13	Sequence 13, Appli
4	104	100.0	798	21 US-10-895-393-9	Sequence 9, Appli
5	104	100.0	806	20 US-10-814-634A-5	Sequence 5, Appli
6	104	100.0	1585	17 US-10-172-118-501	Sequence 501, Appli
7	104	100.0	1585	18 US-10-342-887-501	Sequence 501, Appli

Sequence 1329, Appli

Sequence 19, Appli

Sequence 4, Appli

Sequence 3, Appli

Sequence 4, Appli

Sequence 9, Appli

Sequence 1901, Appli

Sequence 1901, Appli

Sequence 6, Appli

Sequence 6, Appli

Sequence 1, Appli

Sequence 6, Appli

Sequence 17, Appli

Sequence 74, Appli

Sequence 1, Appli

Sequence 2, Appli

Sequence 3, Appli

Sequence 1, Appli

Sequence 34, Appli

Sequence 104, App

Sequence 3, Appli

Sequence 1, Appli

Sequence 33, Appli

Sequence 1, Appli

Sequence 34, Appli

Sequence 3, Appli

Sequence 1, Appli

Sequence 34, Appli

Sequence 3, Appli

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Sequence 34, Appli

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Sequence 34, Appli

Sequence 3, Appli

Sequence 1, Appli

Sequence 34, Appli

Sequence 3, Appli

Sequence 1, Appli

ALIGMENTS

RESULT 1

; Sequence 1, Application US/09801371A-1
 ; Patent No. US2002015559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Osman, Farhat
 ; APPLICANT: Jarrous, Nayef
 ; APPLICANT: Ben-Abouli, Yitzhak
 ; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH MANIPULATION OF mRNA SPLICING AND ITS USES
 ; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
 ; CURRENT APPLICATION NUMBER: US/09/801,371A
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: PCT WO 00/14255
 ; PRIOR FILING DATE: 1999-09-06
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 104
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-801-371A-1

Query Match 100.0%; Score 104; DB 9; Length 104;
 Best Local Similarity 100.0%; Pred. No. 5.2e-28;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGCCCTCCAGACTGGGGCTAACCTGACATCTG 60

Db 1 GAATTCAAACGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG ; PAGES: 6361-6373
; DATE: 1985
; US-10-356-308A-13

Qy 61 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 104
; Query Match 100.0%; Score 104; DB 18; Length 787;
; Best Local Similarity 100.0%; Pred. No. 7.2e-28;
; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 104
; Qy 1 GAATTCAAACGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 60
; Db 222 GAATTCAAACGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 281

Qy 61 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 104
; Db 282 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 325

RESULT 2
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayeef
; APPLICANT: Ben-Aouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF mRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5

Query Match 100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 60
; Db 104 GAATTCAAACGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 45

Qy 61 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 104
; Db 44 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 1

RESULT 3
US-10-356-308A-13
; Sequence 13, Application US/10356308A
; Publication No. US20040039186A1
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall Wilber
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/121-1-CIP1
; CURRENT APPLICATION NUMBER: US/10/356,308A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/032,297
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,266
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 1 to 787
; OTHER INFORMATION: TNFa 3' untranslated region
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E., et al.
; JOURNAL: Nucleic Acid Research
; VOLUME: 13

Query Match 100.0%; Score 104; DB 21; Length 798;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 60
; Db 216 GAATTCAAACGGGGCTCCAGAACTCACTGGGCCCTACAGCTTGTGATCCCTGACATCTG 275

Qy 61 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 104
; Db 276 GAATCTGGAGACCGGGAGCTTGGTTCTGGCCAGAAATGCTGC 319

RESULT 5
US-10-814-634A-5
; Sequence 5, Application US/10814634A
; Publication No. US20040231007A1
; GENERAL INFORMATION:
; APPLICANT: CHENEVAL, Dominique
; APPLICANT: KASTELIC, Tania
; APPLICANT: Novation Pharmaceuticals Inc.
; TITLE OF INVENTION: Assay for Identifying Compounds which
; Affect Stability of mRNA
; FILE REFERENCE: 793-104CIP
; CURRENT APPLICATION NUMBER: US/10/814,634A

RESULT 6
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIORITY APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIORITY APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIORITY APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-342-887-501

Query Match Score 104; DB 20; Length 806;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGACATCTG 60
Db 227 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGACATCTG 286

Qy 61 GAATCTGGAGACCAAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 1.04
Db 287 GAATCTGGAGACCAAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 330

RESULT 6
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIORITY APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 000594
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-501

Query Match Score 104; DB 17; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGACATCTG 60
Db 1003 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTGTGACATCTG 1062

Qy 61 GAATCTGGAGACCAAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 104
Db 1063 GAATCTGGAGACCAAGGGAGCCCTGGTTCTGGCCAGAATGCTGC 1106

RESULT 7
US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:

```

; ; APPLICANT: Ross, F. Patrick
; ; APPLICANT: Teitelbaum, Steven
; ; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; ; FILE REFERENCE: 60019620-0202
; ; CURRENT APPLICATION NUMBER: US/10/272,411
; ; CURRENT FILING DATE: 2002-10-15
; ; PRIOR APPLICATION NUMBER: 60/329,393
; ; PRIOR FILING DATE: 2001-10-15
; ; NUMBER OF SEQ ID NOS: 52
; ; SOFTWARE: PatentIn version 3.1
; ; SEQ ID NO 4
; ; LENGTH: 1643
; ; TYPE: DNA
; ; ORGANISM: Homo sapiens
; ; PUBLICATION INFORMATION:
; ; DATABASE ACCESSION NUMBER: NCBI / X01394.1
; ; DATABASE ENTRY DATE: 1995-03-21
; ; RELEVANT RESIDUES: (1) .. (1643)
; ; PUBLICATION INFORMATION:
; ; DATABASE ACCESSION NUMBER: NCBI / BC028148.1
; ; DATABASE ENTRY DATE: 2002-05-01
; ; RELEVANT RESIDUES: (1) .. (1643)
; ; PUBLICATION INFORMATION:
; ; DATABASE ACCESSION NUMBER: NCBI / M35592.1
; ; DATABASE ENTRY DATE: 1993-04-27
; ; RELEVANT RESIDUES: (1) .. (1643)
; ; PUBLICATION INFORMATION:
; ; DATABASE ACCESSION NUMBER: NCBI / XM_165823.1
; ; DATABASE ENTRY DATE: 2002-08-01
; ; RELEVANT RESIDUES: (1) .. (1643)
; ; US-10-272-411-4
; ; QUERY MATCH 9
; ; Best Local Similarity 100.0%; Pred. No. 8e-28; Length 1585;
; ; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ; Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCAACGCTTGATCCCTGACATCTG 60
; ; Db 1003 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCAACGCTTGATCCCTGACATCTG 1062
; ; Qy 61 GAATCTGGAGACCAGGGAGCCTTGGTTCTGGCCAGAATGCTGC 104
; ; Db 1063 GAATCTGGAGACCAGGGAGCCTTGGTTCTGGCCAGAATGCTGC 1106
; ; RESULT 9
; ; Sequence 19, Application US/10370715B
; ; Publication No. US20040258678A1
; ; GENERAL INFORMATION:
; ; Patic Docket Preview
; ; APPLICANT: BODARY, SARAH C.
; ; APPLICANT: CLARK, HILLARY
; ; APPLICANT: BRISDELL, HUNTER
; ; APPLICANT: JACKMAN, JANET
; ; APPLICANT: SCHOENFELD, JILL R.
; ; APPLICANT: WILLIAMS, P. MICKEY
; ; APPLICANT: WOOD, WILLIAM I.
; ; APPLICANT: WU, THOMAS D.
; ; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; ; Title of Invention: Related Diseases
; ; FILE REFERENCE: P1948R1-US
; ; CURRENT APPLICATION NUMBER: US/10/370,715B
; ; CURRENT FILING DATE: 2003-02-21
; ; NUMBER OF SEQ ID NOS: 742
; ; SEQ ID NO 19
; ; LENGTH: 1585
; ; TYPE: DNA
; ; ORGANISM: Homo sapien
; ; US-10-370-715B-19
; ; QUERY MATCH 11
; ; Best Local Similarity 100.0%; Pred. No. 8e-28; Length 1643;
; ; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ; Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCAACGCTTGATCCCTGACATCTG 60
; ; Db 1070 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCAACGCTTGATCCCTGACATCTG 1129
; ; RESULT 11
; ; US-10-218-547-3
; ; Sequence 3, Application US/10218547
; ; Publication No. US20030100074A1
; ; GENERAL INFORMATION:
; ; APPLICANT: Human Genome Sciences, Inc.
; ; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel.
; ; TITLE OF INVENTION: Human Endokine Alpha
; ; FILE REFERENCE: PF561
; ; CURRENT APPLICATION NUMBER: US/10/218,547
; ; CURRENT FILING DATE: 2002-08-15
; ; PRIOR APPLICATION NUMBER: 60/312,542
; ; PRIOR FILING DATE: 2001-08-16
; ; PRIOR APPLICATION NUMBER: 60/330,761
; ; PRIOR FILING DATE: 2001-10-30
; ; NUMBER OF SEQ ID NOS: 57
; ; SOFTWARE: PatentIn version 3.1
; ; SEQ ID NO 3
; ; LENGTH: 1643
; ; TYPE: DNA
; ; ORGANISM: human
; ; US-10-218-547-3
; ; QUERY MATCH 10
; ; Best Local Similarity 100.0%; Pred. No. 8.e-28; Length 1643;
; ; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ; Qy 1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCAACGCTTGATCCCTGACATCTG 60
; ; Db 1063 GAATCTGGAGACCAGGGAGCCTTGGTTCTGGCCAGAATGCTGC 1106
; ; RESULT 10
; ; US-10-272-411-4
; ; Sequence 4, Application US/10272411
; ; Publication No. US20030100068A1
; ; GENERAL INFORMATION:
; ; APPLICANT: Barnes Jewish Hospital
; ; APPLICANT: Lam, Jonathan

```

RESULT 12
US-10-272-328A-4
; Sequence 4, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-328A-4

Query Match 100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGGCTCCAGAACTCACGGCTTGTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACGGGGCTCCAGAACTCACGGGGCTAACAGCTTGATCCCTGACATCTG 1129

RESULT 14
US-10-172-118-1901
; Sequence 1901, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: X01394
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1901

Query Match 100.0%; Score 104; DB 17; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACGGGGCTCCAGAACTCACGGCTTGTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACGGGGCTCCAGAACTCACGGGGCTAACAGCTTGATCCCTGACATCTG 1129

RESULT 15
US-10-342-887-1901
; Sequence 1901, Application US/10342887

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; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, René
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-342-887-1901

Query Match      100.0%; Score 104; DB 18; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy          1 GAATTCAAACCTGGGCCTCCAGAACTCACTGGGCCAACGCTTTGATCCCTGACATCTG 60
Db          1070 GAATTCAAACCTGGGCCTCCAGAAACTCACTGGGCCAACGCTTTGATCCCTGACATCTG 1129
Qy          61 GAATCTGGAGACCAGGGAGCCTTGGRTCTGCCAGAAATGCTGC 104
Db          1130 GAATCTGGAGACCAGGGAGCCTTGGRTCTGCCAGAAATGCTGC 1173

```

Search completed: September 3, 2005, 00:21:56
 Job time : 484.966 SECs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:55:28 ; Search time 783.946 Seconds
 (without alignments)
 2657.805 Million cell updates/sec

Title: US-09-801-371A-2
 Perfect score: 43
 Sequence: 1 tcaaactggggctccagaa.....actggggccatcacagtttga 43

Scoring table: IDENTITY_NUC
 Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:
 1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_p1:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	43	100.0	400	11	G13533		G13533 SHGC-11076
2	43	100.0	787	6	BD137681	Self-regu	BD137681 Self-regu
3	43	100.0	787	6	AR300453	Sequence	AR300453 Sequence
4	43	100.0	787	6	BD070551	Self-regu	BD070551 Self-regu
5	43	100.0	817	6	A16444	Xho-PstI fr	A16444 Xho-PstI fr
6	43	100.0	817	6	E02109	DNA Sequenc	E02109 DNA Sequenc
7	43	100.0	1047	9	HSA249755		AJ249755 Homo sapi
8	43	100.0	1275	6	10430	Sequence 5	10430 Sequence 5
9	43	100.0	1323	6	107953	Sequence 6	107953 Sequence 6
10	43	100.0	1324	6	E00702	CDNA encodi	E00702 CDNA encodi
11	43	100.0	1324	6	103610	Sequence 2	I03610 Sequence 2
12	43	100.0	1379	12	SYNTNFTRP	M35592 Synthetic h	M35592 Synthetic h
13	43	100.0	1465	6	104244	Sequence 2	104244 Sequence 2
14	43	100.0	1560	6	108863	Sequence 3	108863 Sequence 3
15	43	100.0	1585	6	A37272	Sequence 12	A37272 Sequence 12
16	43	100.0	1585	6	104169	Sequence 1	I04169 Sequence 1
17	43	100.0	1585	6	104198	Sequence 1	I04198 Sequence 1
18	43	100.0	1585	6	108384	Sequence 5	I08384 Sequence 5
19	43	100.0	1585	6	108429	Sequence 3	I08429 Sequence 3

ALIGNMENTS

20	43	100.0	1585	6	AR380784	Sequence	
21	43	100.0	1585	9	HUMTNFAA	M10988 Human tumor	
22	43	100.0	1606	6	107541	Sequence 22	
23	43	100.0	1643	6	AR146199	Sequence	
24	43	100.0	1643	6	AR366225	Sequence	
25	43	100.0	1643	9	HSTNFR	X01394 Human mRNA	
26	43	100.0	1676	9	BC028148	Homo sapi	
27	43	100.0	2270	6	BD137687	Self-regu	
28	43	100.0	2270	6	AR30459	Sequence	
29	43	100.0	2570	6	BD137688	Self-regu	
30	43	100.0	2570	6	AR30460	Sequence	
31	43	100.0	3103	9	HUMTNFX	M262331 Human tumor	
32	43	100.0	3634	6	AR100270	Sequence	
33	43	100.0	3634	6	AR149925	Sequence	
34	43	100.0	3634	6	BD227798	Antisense	
35	43	100.0	3634	6	BD271232	Predictio	
36	43	100.0	3634	6	BD064008	Novel exp	
37	43	100.0	3634	9	HSTNFA	X02910 Human gene	
38	43	100.0	4830	9	AY066019	AY066019 Homo sapi	
39	43	100.0	6974	9	AB088112	Homo sapi	
40	43	100.0	7112	6	AX100950	Sequence	
41	43	100.0	7112	6	AX100965	Sequence	
42	43	100.0	7112	9	HUMTNFAB	M16441 Human tumor	
43	43	100.0	7240	9	AY214167	AY214167 Homo sapi	
C	44	43	100.0	10728	6	AR562497	Sequence
C	45	43	100.0	16310	9	HSTNFBX	Z15026 Homo sapien

CONTACT: Michael Olivier, David R. Cox

Stanford University School of Medicine
 4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA

Tel: (650) 320-5800
 Fax: (650) 320-5801
 Email: Olivier@shgc.stanford.edu
 Primer A: CACTAAGATTCAAACCTGGGC
 Primer B: GAGGAAGGCCCTAAGGTCCAC
 STS size: 166
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds
 Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600
 Protocol:

Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/uL
 Total Vol: 10 uL
 Buffer: Buffer:

RESULTS

RESULT 3
AR300453 2.5 mM
LOCUS 5.0 mM
DEFINITION 20 mM
ACCESSION 8.3 mM
VERSION PAT 12-JUN-2003
KEYWORDS linear
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 787)
AUTHORS Tatake, R.J., Marlin, S.D. and Barton, R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: US 6537784-A 7 25-MAR-2003;
FEATURES Location/Qualifiers
Source 1. .787
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
 Db 226 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 268

RESULT 2
BD137681 787 bp DNA linear PAT 18-SEP-2002
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION BD137681
VERSION BD137681.1 GI:23232626
KEYWORDS JP 2002504381-A/7.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 787)
AUTHORS Tatake, R.J., Marlin, S.D. and Barton, R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: JP 2002504381-A 7 12-FEB-2002;
COMMENT BOEHRINGER INGELHEIM PHARMACEUTICALS INC OS Homo sapiens (human)
 PN JP 2002504381-A/7
 PD 12-FEB-2002
 PF 12-JAN-1999 JP 20000533579
 PR 27-FEB-1998 US 60/076316
 PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC C12N15/09, A61K31/70B8, A61K48/00, A61P1/04, A61P3/10, A61P17/06, PC A61P25/00, PC A61P29/00, A61P43/00, C12N9/64, C12Q1/68//C12N5/10, C12N15/00, CC TNF-alpha untranslated region
 FH Key
 FT source 1. .787
FEATURES Location/Qualifiers
 Source 1. .787
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ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 787;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
 Db 226 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 268

RESULTS

RESULT 4
BD070551 787 bp DNA linear PAT 27-AUG-2002
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION BD070551
VERSION BD070551.1 GI:22616154
KEYWORDS JP 2001516210-A/13.
SOURCE unidentified
ORGANISM unidentified
Unclassified.
REFERENCE 1 (bases 1 to 787)
AUTHORS Tatake, R.J., Marlin, S.D. and Barton, R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: JP 2001516210-A 13 25-SEP-2001;
COMMENT BOEHRINGER INGELHEIM PHARMACEUTICALS INC OS unidentified
 PN JP 2001516210-A/13
 PD 25-SEP-2001
 PF 27-FEB-1998 JP 1998537909
 PR 28-FEB-1997 US 60/039266
 PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC A61K31/70, C07H21/04, C12N15/12, C12P19/34
 CC Strandedness: Single;
 CC Topology: Linear;
 CC TNF alpha nontranslated region
 FH Key
 FT source 1. .787
FEATURES Location/Qualifiers
 Source 1. .787
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 787;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
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ORIGIN /organism="unknown" /mol_type="unassigned DNA"

Query Match 100.0%; Score 43; DB 6; Length 1275;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 43
Db 697 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 739

RESULT 9
LOCUS 107953 1323 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0168214.
VERSION I07953.1 GI:589335
KEYWORDS ·
SOURCE ·
ORGANISM Unknown. Unclassified.

REFERENCE 1 (bases 1 to 1323)
AUTHORS Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.
TITLE Tumor necrosis factor, methods for its preparation, compositions containing it, DNA encoding it and assay method using such DNA
PATENT: EP 0168214-A2 6 15-JAN-1986;
FEATURES ·
SOURCE 1. .1323 /organism="unknown" /mol_type="unassigned DNA"

ORIGIN Query Match 100.0%; Score 43; DB 6; Length 1323;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 43
Db 754 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 796

RESULT 10
LOCUS E00702 1324 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human tumor necrosis factor.
VERSION E00702
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
COMMENT Baraa, B.A., DebitSudo, B.G., San, H.R. and Guren, E.N.

REFERENCE 1 (bases 1 to 1324)
AUTHORS Baraa, B.A., DebitSudo, B.G., San, H.R. and Guren, E.N.
TITLE TUMOR NECROTIC FACTOR
JOURNAL Patent: JP 1986040221-A 1 26-FEB-1986;
GENENTECH INC
OS homosapiens
PN JP 1986040221-A/1
PD 26-FEB-1986
PF 05-JUL-1985 JP 1985149075
PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR
05-JUL-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR
03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454 PI BARAA
BUSHIYAN AGAWARI, DEBITSUDO BANCOMAN GETSUADERU, PI SAN HII RII,
PI GUREN EBAN NEDOUIN
PC A61K35/12, A61K35/02, A61K35/14, A61K35/74, A61K37/04, C07H21/02,
PC C07H21/04,
PC C12N15/00;
CC strandedness: Single;
CC topology: Linear;

ORIGIN Query Match 100.0%; Score 43; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 43
Db 755 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 797

RESULT 11
LOCUS I03610 1324 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4650674.
VERSION I03610
KEYWORDS ·
SOURCE ·
ORGANISM Unknown. Unclassified.

REFERENCE 1 (bases 1 to 1324)
AUTHORS Aggarwal,B.B. and Lee,S.H.
TITLE Synergistic cytotoxic composition
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco, CA
FEATURES ·
SOURCE 1. .1324 /organism="unknown" /mol_type="unassigned DNA"

ORIGIN Query Match 100.0%; Score 43; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 43
Db 755 TCAAACTGGGCCTCCAGAACACTGGGCTTACAGCTTTGA 797

RESULT 12
LOCUS SYNTNFTRP 1379 bp mRNA linear SYN 27-APR-1993
DEFINITION Synthetic human tumor necrosis factor mRNA, complete cds.
VERSION M35592
KEYWORDS tumor necrosis factor.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Nobuhara,M., Kanamori,T., Nagase,Y., Nii,A., Morishita,H.,
Tohyama,J., Andoh,S. and Kurimoto,M.
TITLE The expression of human tumor necrosis factor in E. coli

JOURNAL Nucleic Acids Symp. Ser. 17, 131-134 (1986)
 MEDLINE 87174864
 PUBMED 3031624
 COMMENT Original source text: Altered human leukemic B-cell line Ball-1,
 cDNA to mRNA, clone pM324-346.
 FEATURES source Location/Qualifiers 1..1379
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 CDS 178..879
 /note="synthetic tumor necrosis factor precursor"
 /codon_start=1
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 /protein_id="AAC42098..1"
 /db_xref="GI:209486"
 /translation="MSTESMIRDVELAEEALPKKTPGPGQGSRRCLFLSFLIVAGA
 TTLEFLUHFGVMGPQREEFPRDLSSLISPLAQAVRSSSRPDSKPVAHVVANPQAEGQL
 QWLNRANALLANGVELRDNOLVVPSEGGLYLIYSQVLFKGQGCBSPTHVLLTHTSRIA
 VSYQTKVNLLSAIKSPCQCQRETPEGAEAKPWYEPILGGVFQLEKGDRLSAEINRPDYL
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 mat_peptide 400..876
 /product="synthetic tumor necrosis factor"
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 Best Local Similarity 100.0%; Pred. No. 7e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACCTGGGCCTCCAGAACTCAACTGGGCCTACAGCTTTGA 43
 Db 1100 TCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 1142
 RESULT 13
 I04244 104244 Sequence 2 from Patent US 4677197.
 DEFINITION 104244
 ACCESSION 104244.1 GI:268725
 VERSION 104244.1
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1465)
 AUTHORS Lin, L.S. and Yamamoto, R.
 TITLE Purification method for tumor necrosis factor
 JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
 Cetus Corporation; Emeryville, CA
 FEATURES Location/Qualifiers
 source 1..1465
 /organism="unassigned DNA"
 /mol_type="unassigned DNA"
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 Best Local Similarity 100.0%; Pred. No. 7e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACCTGGGCCTCCAGAACTCAACTGGGCCTACAGCTTTGA 43
 Db 887 TCAAACCTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 929
 RESULT 14
 I08863 108863 Sequence 3 from Patent WO 8806625.
 DEFINITION 108863
 ACCESSION 108863.1 GI:588416
 VERSION .
 KEYWORDS .

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:45:43 ; Search time 131.925 Seconds
 (without alignments)
 1929.494 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43

Sequence: 1 tcaaactgggcctccagaa.....actggggccatcacgttttga 43

Scoring table: IDENTITY_NUC
 Gapov 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

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2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

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8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

ALIGNMENTS

21 43 100.0 1585 1 AAN60557 Sequence
 Aca64836 Human TNF
 Adf76346 Novel hum
 Adi32003 Human cDN
 Ado19587 Human PRO
 Adr24640 Breast ca
 Adp54654 Human PRO
 Aan60446 Sequence
 Aat15424 Human tum
 Aan71307 Sequence
 Aat31021 Human tum
 Abk13195 Human tum
 Aal153712 Tumour ne
 Adc35185 Human cDN
 Ad63904 Human TNF
 Acc57575 Polynucle
 Adr26040 Breast ca
 Acf64375 Human TNF
 Ade25664 Human cDN
 Ad988038 Tumour tr
 Adt08160 Human tum
 Aaz20983 Chimeric
 Aaz20984 Chimeric
 Aav39005 TNF-alpha

RESULTS

RESULT 1
 AAZ99817
 ID AAZ99817 Standard; RNA; 43 BP.
 XX
 AC AAZ99817;
 XX DT 12-JUL-2000 (first entry)
 DE Cis-acting nucleotide sequence derived from human TNF-alpha.
 XX KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
 KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
 KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN WO200014255-A1.
 XX PD 16-MAR-2000.
 XX PF 06-SEP-1999; 99WO-IL000483.
 XX PR 07-SEP-1998; 98IL-00126112.
 XX PR 26-OCT-1998; 98IL-00126757.
 XX PA (YISS) YISSUM RES & DEV CO.
 XX PI Kaempfer R, Osman F, Jarrous N, Ben-Abouli Y;
 XX DR 2000-257000/22.
 XX PT Regulation of gene expression by mRNA splicing is carried out using a cis
 PT -acting nucleotide sequence controlled by phosphorylation of the alpha-
 PT subunit of eukaryotic initiation factor 2.
 XX PS Claim 5, Page 15; 75pp; English.
 XX CC The specification describes a cis-acting nucleotide sequence which is
 CC capable of removing introns from a precursor transcript encoded by a gene
 CC which harbours at least one cis-acting nucleotide sequence. This removal
 CC is effected during the production of mRNA of the gene, and depends on
 CC activation of a trans-acting factor which is an RNA-activated protein
 CC kinase capable of phosphorylating the alpha-subunit of eukaryotic

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	43	3 AAZ99817	Aaz99817 Cis-actin
2	43	100.0	50	3 AAZ99815	Aaz99815 Sequence
3	43	100.0	104	3 AAZ99816	Aaz99816 Cis-actin
4	43	100.0	787	2 AAZ20979	Aaz20979 Human TNF
5	43	100.0	792	13 ADR12297	Adr12297 Human tum
6	43	100.0	815	1 AAN70075	Aan70075 Human ant
7	43	100.0	817	2 AAQ04340	Aaq04340 THP-1. 3 /
8	43	100.0	818	1 AAN91035	Aan91035 Xhol - Ps
9	43	100.0	1200	1 AAN70072	Aan70072 Human ant
10	43	100.0	1200	1 AAN0969	Aan0969 Part of g
11	43	100.0	1275	1 AAN60558	Aan60558 Sequence
12	43	100.0	1279	10 ADE25716	Ade25716 Human cDN
13	43	100.0	1323	1 AAN60363	Aan60363 Sequence
14	43	100.0	1324	3 AAA34963	Aaa34963 Human ade
15	43	100.0	1324	3 AAF21085	Aaf21085 Human low
16	43	100.0	1324	10 ABZ96779	Abz96779 Human nuc
17	43	100.0	1324	11 ABD20628	Abd20628 Human pul
18	43	100.0	1560	1 AAN80219	Aan80219 Sequence
19	43	100.0	1581	12 ADQ83817	Adq83817 Human tum
20	43	100.0	1585	1 AAN60527	Aan60527 Sequence

initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the invention.

SQ Sequence 43 BP; 10 A; 13 C; 11 G; 9 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 3; Length 43;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 43
 Db 1 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 43

RESULT 2
 AAZ99815
 ID AAZ99815 standard; RNA; 50 BP.
 XX
 AC AAZ99815;
 XX DT 12-JUL-2000 (First entry)
 DE Sequence of the stem loop of tumour necrosis factor-alpha gene.
 XX KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
 KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
 KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
 XX OS Homo sapiens.
 PN WO200014255-A1.
 XX PD 16-MAR-2000.
 XX PR 06-SEP-1999; 99WO-IL000483.
 XX PR 07-SEP-1998; 98IL-00126112.
 XX PR 26-OCT-1998; 98IL-00126757.
 XX PA (YISS) YISSUM RES & DEV CO.
 PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
 XX DR WPI; 2000-257000/22.

XX PR 07-SEP-1998; 98IL-00126112.
 XX PR 26-OCT-1998; 98IL-00126757.
 XX PA (YISS) YISSUM RES & DEV CO.
 PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
 XX DR WPI; 2000-257000/22.

XX PS Example 7; Fig 5B; 75pp; English.
 XX The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the invention.

XX SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 3; Length 104;
 CC CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a fragment of the human TNF-alpha

CC CC protein) or agriculturally applicable protein. The present sequence represents a fragment of the 3'UTR of human TNF-alpha
 XX SQ Sequence 50 BP; 12 A; 15 C; 12 G; 0 T; 11 U; 0 Other;
 Query Match 100.0%; Score 43; DB 3; Length 50;
 Best Local Similarity 79.1%; Pred. No. 4.4e-07;
 Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 43
 Db 5 UCAAACTGGGCCUCCAGAACUACUGGGCTUACAGCTUUGA 47

RESULT 3
 AAZ99816
 ID AAZ99816 standard; RNA; 104 BP.
 XX
 AC AAZ99816;
 XX DT 12-JUL-2000 (First entry)
 DE Cis-acting nucleotide sequence derived from human TNF-alpha.
 XX KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
 KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
 KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN WO200014255-A1.
 XX PD 16-MAR-2000.
 XX PR 06-SEP-1999; 99WO-IL000483.
 XX PR 07-SEP-1998; 98IL-00126112.
 XX PR 26-OCT-1998; 98IL-00126757.
 XX PA (YISS) YISSUM RES & DEV CO.
 PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
 XX DR WPI; 2000-257000/22.

XX PR 06-SEP-1999; 99WO-IL000483.
 XX PD 16-MAR-2000.
 XX PR 07-SEP-1998; 98IL-00126112.
 XX PR 26-OCT-1998; 98IL-00126757.
 XX PA (YISS) YISSUM RES & DEV CO.
 PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
 XX DR WPI; 2000-257000/22.

XX PS Example 7; Fig 5B; 75pp; English.
 XX The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the invention.

XX SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 3; Length 104;

Anti-tumor; cancer; cytotoxic; 88.	
Homo sapiens.	
OS XX	Used in the prodn. of TNF prodn. agents. (Updated on 25-MAR-2003 to correct PD field.)
XX PN XX	
XX EP247906-A.	
XX 02-DEC-1987.	
XX 04-FEB-1987; 87EP-00400261.	
XX PF XX	
XX PR XX	
XX PR 04-FEB-1986; 86JP-00021302.	
XX PR 07-FEB-1986; 86JP-00024220.	
XX PR 17-JUL-1986; 86JP-00169522.	
XX PA XX	(MIZU/) MIZUNO D.
XX PI XX	Mizuno D, Soma GI;
XX DR XX	WPI; 1987-336540/48.
XX PT XX	Anti-tumour polypeptide(s) - prepd. using recombinant DNA prepd. from genomic DNA of human acute leukaemia cell thp-1.
XX PT XX	Disclosure; Fig 7; 63pp; English.
XX PS XX	The sequence is an Xho-PstI fragment of an anti-tumor protein. The polypeptide is cytotoxic to human tumor cells but not to normal cells. They are also cytotoxic to primary cell cultures obtained from metastasis lesions of patients suffering from striated muscle tumors. They are also resistant to all chemotherapeutic agents. See also AAN70073-74, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ XX	Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 U; 0 Other;
XX Query Match XX	100.0%; Score 43; DB 1; Length 815;
XX Best Local Similarity XX	100.0%; Pred. No. 6.8e-07;
XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX QY XX	1 TCAGAACTGGGCCCTCAGAACTCACTGGGCCCTACAGCTTGA 43
XX Db XX	716 TCAGAACTGGGCCCTCAGAACTCACTGGGCCCTACAGCTTGA 758
XX RESULT 7 XX	
XX ID XX	AAQ04340 Standard; DNA; 817 BP.
XX AC XX	AAQ04340;
XX DT XX	25-MAR-2003 (revised)
XX DT XX	21-SEP-1990 (first entry)
XX SQ XX	Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 U; 0 Other;
XX DE XX	THP-1.
XX Acute leukaemia cell; THP-1; anti-tumour agent; ss.	
XX Homo sapiens.	
XX PN XX	JP02088598-A.
XX PD XX	28-MAR-1990.
XX PF XX	22-SEP-1988; 88JP-00239154.
XX PR XX	22-SEP-1988; 88JP-00239154.
XX PA XX	(SOMA/) SOMA G.
XX DR XX	WPI; 1990-143138/19.
XX PT XX	Intrinsic TNF prodn. derivation agents - contain primer and trigger, at least one of which has TNF activity.
XX PT XX	PT
PS Disclosure; Page ?; 26pp; Japanese.	
XX CC CC	
XX CC CC	
SQ Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 U; 0 Other;	
Query Match 100.0%; Score 43; DB 2; Length 817;	
Best Local Similarity 100.0%; Pred. No. 6.8e-07;	
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 TCAGAACTGGGCCCTCAGAACTCACTGGGCCCTACAGCTTGA 43	
Db 716 TCAGAACTGGGCCCTCAGAACTCACTGGGCCCTACAGCTTGA 758	
XX RESULT 8 XX	
XX ID XX	AAN91035
XX AC XX	AAN91035;
XX DT XX	27-AUG-2003 (revised)
XX DT XX	11-MAR-1990 (first entry)
XX DE XX	XhoI - PstI Section of gene for anti-cancer peptide.
XX KW XX	Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX KW XX	THP 1 cells.
XX OS XX	OS
XX PN XX	JP01095784-A.
XX PD XX	13-APR-1989.
XX PF XX	06-OCT-1987; 87JP-00252174.
XX PR XX	06-OCT-1987; 87JP-00252174.
XX PA XX	(SENG/) SEN G.
DR WPI; 1989-154899/21.	
XX PT PT	Novel DNA, plasmid and polypeptide(s) - useful as anticarcinogenic agents.
XX XX	Fig 3; Page ?; 17pp; Japanese.
PS XX	
XX CC CC	Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1 cells. (Updated on 27-AUG-2003 to correct OS field.)
XX CC CC	
SQ Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 U; 0 Other;	
Query Match 100.0%; Score 43; DB 1; Length 818;	
Best Local Similarity 100.0%; Pred. No. 6.8e-07;	
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 TCAGAACTGGGCCCTCAGAACTCACTGGGCCCTACAGCTTGA 43	
Db 717 TCAGAACTGGGCCCTCAGAACTCACTGGGCCCTACAGCTTGA 759	
XX RESULT 9 XX	
XX ID XX	AAN70072
XX AC XX	AAN70072;
XX DT XX	25-MAR-2003 (revised)
XX DT XX	20-JAN-1991 (first entry)
XX DE XX	Human anti-tumor polypeptide.

KW Anti-tumor; cancer; cytotoxic; **BB**.
 XX PS Fig 2; Page ?; 17pp; Japanese.
 OS XX Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1
 XX cells. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-
 PN CC 2003 to correct OS field.)
 XX CC
 PD CC
 XX CC
 PP 04-FEB-1987; 87EP-00400261.
 XX SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 1; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGA 43
 Db 1099 TCAAACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGA 1141

RESULT 11
 XX AAN60558
 ID AAN60558 Standard; DNA; 1275 BP.
 AC AAN60558;
 PS XX DT 28-JUL-1991 (first entry)
 PA XX DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser
 XX DE 69 in PAW731.
 PA (MIZUNO) MIZUNO D.
 XX DE Antitumour; anticancer; **BB**.
 PI Mizuno D, Soma GI;
 XX KW
 DR WPI; 1987-336540/48.
 XX PS Disclosure; Fig 4; 63pp; English.
 PT PT Anti-tumour polypeptide(s) - prep'd. using recombinant DNA prepd. from
 PT genomic DNA of human acute leukaemia cell thp-1.
 XX PS
 CC The polypeptide is cytotoxic to human tumor cells but not to normal
 CC cells. They are also cytotoxic to primary cell cultures obtained from
 CC metastasis lesions of patients suffering from striated muscle tumors.
 CC They are also resistant to all chemotherapeutic agents. See also AAN70073
 CC -75, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR
 CC field.)
 XX SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 1; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGA 43
 Db 1099 TCAAACTGGGCCCTCCAGAACTCACTGGGCCCTACAGCTTGA 1141

RESULT 10
 XX AAN90969
 ID AAN90969 Standard; DNA; 1200 BP.
 AC AAN90969;
 XX DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 11-MAR-1990 (first entry)
 XX DE Part of gene for anti-cancer peptide.
 KW OS THP 1 cells.
 XX Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
 OS
 XX JP01095784-A.
 PN 13-APR-1989.
 PD 06-OCT-1987; 87JP-00252174.
 XX 06-OCT-1987; 87JP-00252174.
 PR PA (SENG/) SEN G.
 XX DR WPI; 1989-154899/21.
 XX PT Novel DNA, plasmid and polypeptide(s) - useful as anticarcinogenic
 PT agents.

XX SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 1; Length 1275;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 43
 Db 697 TCAAACGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 739

RESULT 12
ADE25716 Standard; cDNA; 1279 BP.

XX ADE25716;
 AC XX DT 29-JAN-2004 (First entry)
 DE Human cDNA differentially expressed in foam cells #120.
 XX KW Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;
 KW cardiovascular disease; atherosclerosis.
 XX OS Homo sapiens.
 PN US2003194721-A1.
 XX PD 16-OCT-2003.
 XX PF 18-SEP-2002; 2002US-00247671.
 XX PR 19-SEP-2001; 2001US-0323784P.
 PA (INCY-) INCYTE GENOMICS INC.
 PI Mikita T, Shiffman D, Porter JC, Kaser MR;
 XX WPI; 2003-875398/81.
 DR DR-P-PSDB; ADE25778.
 XX PT Combination containing several polynucleotide that are differentially
 PT expressed in foam cells and complements of the polynucleotides, useful
 PT for diagnosing cardiovascular disease or atherosclerosis.
 PS Claim 1; SEQ ID NO 120; 37pp; English.
 XX The invention relates to a combination comprising several polynucleotides
 having any one of 127 sequences (S1) such as the sequence of human
 calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4
 hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit
 mRNA, etc., and their complements. The cDNAs are differentially expressed
 in LPS (lipopolysaccharide)-treated foam cells. Also included are
 obtaining an extended or full length gene from a library of nucleic acid
 sequences, an expression vector containing the nucleic acids, a host cell
 containing the vector, a purified polypeptide appearing as ADE25750 and
 ADE25751, producing a protein by culturing the host cell, and a
 composition comprising a purified antibody that specifically binds to the
 protein. The foam cell-expressed nucleic acids are useful for a high
 throughput detection of differential expression of one or more
 polynucleotides in a sample. The sample is from a subject with
 atherosclerosis and comparison with a standard defines early, mid or late
 stages of the disorder. The foam cell-expressed nucleic acids are useful
 for high throughput screening of a library of molecules or compounds to
 identify a ligand which binds a polynucleotide. The library is chosen
 from DNA molecules, peptides, proteins and RNA molecules. The protein is
 useful for a high throughput screening of library of molecules or
 compounds to identify at least one ligand which specifically binds a
 protein, for purifying a ligand from a sample for making a antibody. The
 foam cell-expressed nucleic acids are useful for diagnosing
 cardiovascular disorder. The foam cell-expressed nucleic acids are useful
 as elements on a microarray which can be used for detecting related
 polynucleotide in a sample, diagnosing cardiovascular disease,
 atherosclerosis. The present sequence represents a cDNA whose expression
 is upregulated in LPS treated foam cells.
 XX SQ Sequence 1279 BP; 293 A; 415 C; 323 G; 248 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 43; DB 1; Length 1323;
 Best Local Similarity 100.0%; Pred. No. 7.4e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 43
 Db 1081 TCAAACGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 1123

RESULT 13
AAN60363 Standard; DNA; 1323 BP.

XX ID AAN60363
 AC XX DT 19-JUN-1991 (first entry)
 DE Sequence encoding human tumour necrosis factor.
 XX KW hTNF; tumour; cancer; interferon; ds.
 OS Homo sapiens.
 XX KEY FH Location/Qualifiers
 CDS 1..534 /*tag= a
 FT sig_peptide 1..60 /*tag= b
 FT mat_peptide 61..534 /*tag= c
 FT PR 03-JUL-1985; 85EP-00304758.
 XX PR 05-JUL-1984; 84US-00627959.
 PR 05-JUL-1984; 84US-00628059.
 PR 05-JUL-1984; 84US-00628060.
 PR 05-JUL-1984; 84US-00677156.
 PR 03-DEC-1984; 84US-00677257.
 PR 03-DEC-1984; 84US-00677267.
 PR 03-DEC-1984; 84US-00677454.
 PA (GETH) GENENTECH INC.
 XX PI Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;
 DR WPI; 1986-015483/03.
 DR P-PSDB; AAP60417.

XX Pure tumour necrosis factor and mutant forms - new DNA coding sequences
 and transformed cells.
 XX Claim 20; Fig 10; 90pp; English.

PS Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;
 XX CC Sequence encodes the pure human tumour necrosis factor, mutants of which
 CC are covered by the claims. TNF and mutants are useful in treating
 CC tumours, especially in tandem with interferon. The encoding sequence may
 CC be used to create plasmid pTRXAPTNF, allowing transformation of an
 CC E.coli host for the expression of TNF
 XX SQ Query Match 100.0%; Score 43; DB 1; Length 1323;
 Best Local Similarity 100.0%; Pred. No. 7.4e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 43
 Db 754 TCAAACGGGCCTCCAGAACTCACTGGGCCTACAGCTTGA 796

Query Match 100.0%; Score 43; DB 10; Length 1279;

CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention

XX Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 3; Length 1324;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACGGGCCTCCAGAACACTGCGGCCTACAGCTTGA 43
Db 755 TCAAACGGGCCTCCAGAACACTGGGCCTACAGCTTGA 797

Search completed: September 3, 2005, 00:29:35
Job time : 132.925 secs

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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 23:36:03 ; Search time 983.15 Seconds
 (without alignments)
 1664.816 Million cell updates/sec

Title: US-09-801-371A-2
 Perfect score: 43
 Sequence: 1 tcaaactggggccctccagaa.....actggggccatcacagtttga 43

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_htc:
 4: gb_est3:
 5: gb_est4:
 6: gb_est5:
 7: gb_est6:
 8: gb_gss1:
 9: gb_gss2:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	43	100.0	248	7	T29839		T29839 EST97164 Hu	
2	43	100.0	474	5	BX118951		BX118951 BX118951	
C	3	100.0	630	6	CB528492		CB528492 UI-H-FT2-	
C	4	100.0	645	6	CD370363		CD370363 UI-H-FT1-	
C	5	100.0	684	6	CA307429		CA307429 UI-H-FT1-	
C	6	100.0	688	6	CD367676		CD367676 UI-H-FT1-	
C	7	100.0	696	6	CA307225		CA307225 UI-H-FT1-	
C	8	100.0	699	6	CD364761		CD364761 UI-H-FT2-	
C	9	100.0	703	6	CD368142		CD368142 UI-H-FT1-	
C	10	43	100.0	713	6	CA308256		CA308256 UI-H-FT1-
C	11	43	100.0	719	6	CB528694		CB528694 UI-H-FT2-
C	12	43	100.0	722	5	BQ007008		BQ007008 UI-H-EI1-
C	13	43	100.0	722	6	CA307062		CA307062 UI-H-FT1-
C	14	43	100.0	722	6	CD364988		CD364988 UI-H-FT2-
C	15	43	100.0	723	6	CA308777		CA308777 UI-H-FT1-
C	16	43	100.0	723	6	CD368116		CD368116 UI-H-FT1-
C	17	43	100.0	724	6	CA309711		CA309711 UI-H-FT1-
C	18	43	100.0	726	6	CA310368		CA310368 UI-H-FT1-
C	19	43	100.0	726	6	CD368929		CD368929 UI-H-FT1-
C	20	43	100.0	742	6	CA309509		CA309509 UI-H-FT1-
C	21	43	100.0	744	6	CD366187		CD366187 UI-H-FT1-
C	22	43	100.0	748	6	CA306559		CA306559 UI-H-FT1-
C	23	43	100.0	755	6	CD240146		CD240146 DTL3P2G5
C	24	43	100.0	1068	1	AL543083		AL543083 AL543083

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	43	100.0	248	7	T29839		T29839 EST97164 Hu	
2	43	100.0	474	5	BX118951		BX118951 BX118951	
C	3	100.0	630	6	CB528492		CB528492 UI-H-FT2-	
C	4	100.0	645	6	CD370363		CD370363 UI-H-FT1-	
C	5	100.0	684	6	CA307429		CA307429 UI-H-FT1-	
C	6	100.0	688	6	CD367676		CD367676 UI-H-FT1-	
C	7	43	100.0	696	6	CA307225		CA307225 UI-H-FT1-
C	8	43	100.0	699	6	CD364761		CD364761 UI-H-FT2-
C	9	43	100.0	703	6	CD368142		CD368142 UI-H-FT1-
C	10	43	100.0	713	6	CA308256		CA308256 UI-H-FT1-
C	11	43	100.0	719	6	CB528694		CB528694 UI-H-FT2-
C	12	43	100.0	722	5	BQ007008		BQ007008 UI-H-EI1-
C	13	43	100.0	722	6	CA307062		CA307062 UI-H-FT1-
C	14	43	100.0	722	6	CD364988		CD364988 UI-H-FT2-
C	15	43	100.0	723	6	CA308777		CA308777 UI-H-FT1-
C	16	43	100.0	723	6	CD368116		CD368116 UI-H-FT1-
C	17	43	100.0	724	6	CA309711		CA309711 UI-H-FT1-
C	18	43	100.0	726	6	CA310368		CA310368 UI-H-FT1-
C	19	43	100.0	726	6	CD368929		CD368929 UI-H-FT1-
C	20	43	100.0	742	6	CA309509		CA309509 UI-H-FT1-
C	21	43	100.0	744	6	CD366187		CD366187 UI-H-FT1-
C	22	43	100.0	748	6	CA306559		CA306559 UI-H-FT1-
C	23	43	100.0	755	6	CD240146		CD240146 DTL3P2G5
C	24	43	100.0	1068	1	AL543083		AL543083 AL543083

RESULT 1

LOCUS	DEFINITION
T29839	EST97164 Human Testis Homo sapiens cDNA 5' end similar to tumor necrosis factor, alpha (HT:1190), mRNA sequence.
T29839	EST:
T29839.1	GI:611937
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 248)
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Hinkley, P.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Kelley, J.C., Hedblom, E., Mermick, J.M., Moreno-Palangues, R.F., McDonald, L.A., Pellegrino, S.M., Phillips, C.A., Rydell, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Koza, D.L., Kunsch, C., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Rubin, S.M., Dillon, P.J., Fannon, M.R., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
TITLE	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL	Nature 377, 3-174 (1995)
MEDLINE	96026280
PUBMED	7566098
COMMENT	Contact: Venter, J.C. The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1. 248
 FEATURES
 Source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):107667"
 /db_xref="taxon:9606"
 /clone_lib="Human Testis"
 /note="Organ: testis"

ORIGIN

Query Match 100.0%; Score 43; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAACACTGGGCCCTACAGCTTGA 43
 Db 62 TCAAACGGGCCTCCAGAACACTGGGCCCTACAGCTTGA 104

RESULT 2
 BX118951 LOCUS BX118951 Soares_fetal_heart_NbHL19W Homo sapiens cDNA clone
 DEFINITION IMAGP998L124300 ; IMAGE:1693595 mRNA sequence.
 ACCESSION BX118951
 VERSION BX118951.1 GI:27882696
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 COMMENT 1 (bases 1 to 474)
 REFERENCE Ebert,L., Heil,O., Henning,S., Neubert,P., Partsch,B., Peters,M., Radelof,U., Schneider,D. and Korn,B.
 AUTHORS Human UniGeneSet - RZPD3
 TITLE Unpublished (2003)
 JOURNAL Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGP998L124300.
 RZPDLIB; I.M.A.G.E. Clone Collection;
 Human UniGeneSet - RZPD3 (RZPDLIB No. 972)
 http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

This clone is available royalty-free from RZPD; Contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGAAAACAGCTATGAC.

FEATURES source

1. .474 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGP998L124300 ; IMAGE:1693595"
 /sex="unknown"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal heart_NbHL19W"
 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGATCTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

FEATURES source

1. 630 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT2-bjd-e-20-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT2"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University

ORIGIN

of Iowa.
 TAG TISSUE=Human Lung Alveolar Macrophage
 TAG LIB=UI-H-FT1
 TAG SEQ=GCCATGCCG"

ORIGIN

Query Match Score 43; DB 6; Length 630;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACCTGGGCCTCCAGAACTCACTGGGCTTACAGCTTGA 43
 Db 499 TCAAACCTGGGCCTCCAGAACTCACTGGGCTTACAGCTTGA 457

RESULT 4

CD370363/c
 LOCUS CD370363
 DEFINITION UI-H-FT1-bkb-n-03-0-UI.81 NCI CGAP FT1 Homo sapiens cDNA clone
 ACCESSION CD370363
 VERSION CD370363.1 GI:31154453
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 645)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgaps-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>

The following repetitive elements were found in this cDNA
 Sequence: 294-368, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source

1. 645
 /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3

hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lennon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor,
 digested with Not I, and cloned directionally into
 pTR7T3-Pac vector. The Oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 GGCCATGCCG. The tissue was provided by Dr. Gary W.
 Hunninghake of the University of Iowa.
 TAG TISSUE=Human Lung Alveolar Macrophage
 TAG LIB=UI-H-FT1
 TAG SEQ=GGCCATGCCG"

ORIGIN

Query Match Score 43; DB 6; Length 645;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACCTGGGCCTCCAGAACTCACTGGGCTTACAGCTTGA 43
 Db 588 TCAAACCTGGGCCTCCAGAACTCACTGGGCTTACAGCTTGA 546

RESULT 5
 CA307429/c
 LOCUS CA307429
 DEFINITION UI-H-FT1-bic-i-01-0-UI.81 NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-bic-i-01-0-UI 3', mRNA sequence.
 ACCESSION CA307429
 VERSION CA307429.1 GI:24470483
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 684)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 The following repetitive elements were found in this cDNA
 Sequence: 294-368, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source

Location/Qualifiers
 1. 684
 /organism="Homo sapiens"
 /mol type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bkb-n-03-0-UI"
 /tissue type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone.lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3

the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTR73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	100.0%	Score 43;	DB 6;	Length 684;
Best Local Similarity	100.0%	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 591 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 549

RESULT 6

CD367676/c

LOCUS CD367676 688 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bjr-1-14-0-UI .s1 NCI CGAP FT1 Homo sapiens CDNA clone
UI -H-FT1-bjr-1-14-0-UI 3', mRNA sequence.
VERSION CD367676.1 GI:31151766
KEYWORDS EST.
ORGANISM Homo sapiens (human)

RESULT 7
CA307225/c
LOCUS CA307225
DEFINITION UI-H-FT1-bhu-n-04-0-UI .s1 NCI CGAP FT1 Homo sapiens CDNA clone
UI -H-FT1-bhu-n-04-0-UI 3', mRNA sequence.
VERSION CA307225
KEYWORDS EST.
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 688)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/nicigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this CDNA
Sequence: 69-143, >(TAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1. .688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjr-1-14-0-UI"
/tissue_type="Alveolar Macrophage"

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 43
Db 363 TCAAACCTGGGCCTCCAGAACACTCACTGGGCCTACAGCTTTGA 321

ORIGIN

Query Match	100.0%;	Score 43;	DB 6;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 2.9e-05;		
Matches	43;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;	

Qy 1 TCAAACCTGGGCCTCC

The following repetitive elements were found in this CDNA sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES SOURCE	TITLE	JOURNAL	COMMENT
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D. Email: cgaps@rmail.nih.gov
			Tissue Procurement: Dr. Gary W. Hunninghake, U of I CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html The following repetitive elements were found in this CDNA sequence: 296-370, >(TAAA)n#Simple_repeat
Location/Qualifiers			Seq primer: M13 FORWARD POLYA=Yes.
FEATURES SOURCE	FEATURES SOURCE	LOCATION/QUALIFIERS	LOCATION/QUALIFIERS
1. :696 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-H-FT1-bhu-n-04-0-UI" /tissue_type="Alveolar Macrophage" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI CGAP FT1" /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into PT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT1 TAG_SEQ=GGCCATGCCG"			
ORIGIN			
	Query Match 100.0%; Score 43; DB 6; Length 696; Best Local Similarity 100.0%; Pred. No. 2.9e-05; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ORIGIN	
Qy	1 TCAAACCTGGGCCTCCAGAACACTGGGGCTACAGCTTGA 43 Db 590 TCAAACCTGGGCCTCCAGAACACTGGGGCTACAGCTTGA 548		
		Query Match 100.0%; Score 43; DB 6; Length 699; Best Local Similarity 100.0%; Pred. No. 2.9e-05; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 8 CD364761/c	1 TCAAACCTGGGCCTCCAGAACACTGGGGCTACAGCTTGA 43 Db 590 TCAAACCTGGGCCTCCAGAACACTGGGGCTACAGCTTGA 548	Query Match 100.0%; Score 43; DB 6; Length 699; Best Local Similarity 100.0%; Pred. No. 2.9e-05; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
LOCUS CD364761	699 bp mRNA linear EST 05-AUG-2004	Query Match 100.0%; Score 43; DB 6; Length 696; Best Local Similarity 100.0%; Pred. No. 2.9e-05; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 9 CD368142/c
DEFINITION UI-H-FT2-bjm-j-11-0-UI-81 NCI CGAP FT1 Homo sapiens CDNA clone			LOCUS CD368142
VERSION CD364761			DEFINITION UI-H-FT1-bjv-e-20-0-UI-81 NCI CGAP FT1 Homo sapiens CDNA clone
KEYWORDS Homo sapiens (human)			ACCESSION CD368142
SOURCE Homo sapiens			VERSION CD368142.1
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 699)			KEYWORD EST.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/niccgap			SOURCE Homo sapiens (human)
AUTHORS			ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/niccgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
Sequence: 298-372, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES source

1. .703
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bjv-e-20-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a
 modified polylinker; site:1: Ecor I; Site 2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lennon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor,
 digested with Not I, and cloned directionally into
 pT7T3-Pac vector. The oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 GGCCATGCCG. The tissue was provided by Dr. Gary W.
 Hunninghake of the University of Iowa.
 TAG TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT1
 TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match Score 43; DB 6; Length 703;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
 Db 592 TCAAACGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 550

RESULT 10
 CA308256/c
 LOCUS CA308256 linear EST 05-AUG-2004
 DEFINITION UI-H-FT1-bhy-e-14-0-UI..SI NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-bhy-e-14-0-UI 3', mRNA sequence.
 ACCESSION CA308256
 VERSION CA308256.1 GI:24471310
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 713)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/niccgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 296-370, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source

1. .713
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bhy-e-14-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; site:1: Ecor I; Site 2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lennon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor,
 digested with Not I, and cloned directionally into
 pT7T3-Pac vector. The oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 GGCCATGCCG. The tissue was provided by Dr. Gary W.
 Hunninghake of the University of Iowa.
 TAG TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT1
 TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match Score 43; DB 6; Length 703;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
 Db 592 TCAAACGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 550

TAG TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT1

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 590 TCAAACGTGGGCCTCCAGAACACTCAGCTTGA 43

RESULT 11
LOCUS CB528694 719 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT2-bjd-1-22-0-UI..\$1 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.

ACCESSION CB528694
VERSION CB528694.1 GI:29388630
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 719)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
Sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes

FEATURES

source

Location/Qualifiers

1. .719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjd-1-22-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lib="NCI CGAP FR2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.

The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGCCTCCAGAACACTCAGCTTGA 43

Db 588 TCAAACGTGGGCCTCCAGAACACTCAGCTTGA 546

RESULT 12
LOCUS BQ007008/c
DEFINITION UI-H-EII-azb-j-22-0-UI..\$1 NCI CGAP_EII Homo sapiens cDNA clone
IMAGE:5846517 3', mRNA sequence.

ACCESSION BQ007008
VERSION BQ007008.1 GI:19731908
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 722)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS NCI-CGAP Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes

Location/Qualifiers

1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NCI CGAP EII"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lib="NCI CGAP EII"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP_EII is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an Oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACCTGGCAC.

TAG_LIB=UI-H-EII
TAG_SEQ=ACACCTGGCAC"

ORIGIN

Query Match 100.0%; Score 43; DB 5; Length 722;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCTCCAGAACACTGGGCCTACAGCTTGA 43
 Db 591 TCAAACCTGGGCCTCCAGAACACTGGGCCTACAGCTTGA 549

RESULT 13
 CA307062/c

LOCUS 722 bp mRNA linear EST 05-AUG-2004
 DEFINITION NCI-FT1-bhu-o-04-0-UI.81 NCI CGAP_FT1 Homo sapiens CDNA clone
 UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.

ACCESSION CA307062
 VERSION CA307062.1 GI:24470116
 SOURCE EST.
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 722)

REFERENCE 1
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)
 JOURNAL Tumor Gene Index
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this CDNA
 sequence: 295-369, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source
 Location/Qualifiers
 1. 722 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bhu-o-04-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI CGAP FT1 is a normalized CDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV EGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV EGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lemmon and Soares, Genome
 Research, 6:791-806, 1996. First strand CDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded CDNA was ligated to an EcoR I adaptor,

RESULT 14
 CD364988/c

LOCUS 722 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-FT2-bjn-c-04-0-UI.81 NCI CGAP FT2 Homo sapiens CDNA clone
 UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.

ACCESSION CD364988
 VERSION CD364988.1 GI:31149078
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 722)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS NCI-CGAP
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)
 JOURNAL Tumor Gene Index
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/cgap.html
 The following repetitive elements were found in this CDNA
 sequence: 297-371, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source
 Location/Qualifiers
 1. 722 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT2-bjn-c-04-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT2"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI CGAP FT2 is a subtracted cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV EGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV EGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lemmon and Soares, Genome
 Research, 6:791-806, 1996. First strand CDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded CDNA was ligated to an EcoR I adaptor,"

moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT2

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	100.0%	Score 43;	DB 6;	Length 722;
Best Local Similarity	100.0%	Pred. No.	2.9e-05;	
Matches	43;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCTCCAGAACCTCAACTGGGCCTACAGCTTGA 43
Db 591 TCAAACCTGGGCCTCCAGAACCTCAACTGGGCCTACAGCTTGA 549

RESULT 15

CA308777/c

LOCUS CA308777 723 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bhy-b-23-0-UI..81 NCI CGAP_FT1 Homo sapiens CDNA clone
VERSION UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.

ACCESSION

CA308777

VERSION

CA308777.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

REFERENCE

1 (bases 1 to 723)

AUTHORS

NCI-CGAP

<http://www.ncbi.nlm.nih.gov/ngcicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Tissue Procurement:

Dr. Gary W. Hunninghake, U of I

CDNA Library Preparation:

Dr. M. Bento Soares, University of Iowa

DNA Sequencing by:

Dr. M. Bento Soares, University of Iowa

Clone Distribution:

Clone distribution information can be obtained

From:

Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

Sequence: 297-371, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. .723

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FT1-bhy-b-23-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_id="NCI CGAP FT1"

/note="Organ: Lung; Vector: PT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I; NCI CGAP FT1 is a normalized CDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different

conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pR7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	100.0%	Score 43;	DB 6;	Length 723;
Best Local Similarity	100.0%	Pred. No.	2.9e-05;	
Matches	43;	Mismatches	0;	
		Conservative	0;	
		Matches	43;	
		Mismatches	0;	
		Indels	0;	
		Gaps	0;	

Qy 1 TCAAACCTGGGCCTCCAGAACCTCAACTGGGCCTACAGCTTGA 43
Db 591 TCAAACCTGGGCCTCCAGAACCTCAACTGGGCCTACAGCTTGA 549

Query Match 100.0%; Score 43; DB 6; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCTCCAGAACCTCAACTGGGCCTACAGCTTGA 43
Db 591 TCAAACCTGGGCCTCCAGAACCTCAACTGGGCCTACAGCTTGA 549

Search completed: September 3, 2005, 02:11:42
Job time : 985.15 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: September 2, 2005, 13:14:57 ; Search time 175.51 Seconds
 (without alignments)
 400.888 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43

Sequence: 1 tcaaactgggcctccagaa.....actggggccatcacgcttga 43

Scoring table: IDENTITY_NUC

GapOp 10_0 , GapExt 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:
 1: /cggn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cggn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cggn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cggn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cggn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cggn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	43	100.0	787	4	US-09-032-297A-13		Sequence 13, Appl	
2	43	100.0	787	4	US-09-229-151C-7		Sequence 7, Appl	
3	43	100.0	1585	4	US-09-023-655-1329		Sequence 1329, Ap	
4	43	100.0	1587	4	US-09-949-016-5156		Sequence 5156, Ap	
5	43	100.0	1643	3	US-08-880-342-36		Sequence 36, Appl	
6	43	100.0	1643	3	US-09-505-250-4		Sequence 4, Appl	
7	43	100.0	2270	4	US-09-229-151C-13		Sequence 13, Appl	
8	43	100.0	2570	4	US-09-229-151C-14		Sequence 14, Appl	
9	43	100.0	3634	3	US-09-166-186-1		Sequence 1, Appl	
10	43	100.0	3634	3	US-09-313-932-1		Sequence 1, Appl	
11	43	100.0	3634	3	US-09-109-663-34		Sequence 34, Appl	
12	43	100.0	6682	4	US-09-949-016-16898		Sequence 16898, A	
C	13	43	100.0	10728	4	US-09-376-774-5		Sequence 5, Appl
C	14	23	53.5	11752	4	US-09-949-016-11756		Sequence 11756, A
C	15	23	53.5	11865	4	US-09-949-016-15297		Sequence 15297, A
C	16	23	53.5	11865	4	US-09-949-016-15298		Sequence 15298, A
C	17	23	53.5	33753	4	US-09-949-016-15741		Sequence 15741, A
C	18	23	53.5	33756	4	US-09-949-016-12006		Sequence 12006, A
C	19	21.4	49.8	601	4	US-09-949-016-137730		Sequence 137730,
C	20	21.4	49.8	601	4	US-09-949-016-137731		Sequence 137731,
C	21	21.4	49.8	1274	4	US-09-148-545-72		Sequence 72, Appl
C	22	21.4	49.8	1296	4	US-09-148-545-126		Sequence 126, App
C	23	21.4	49.8	24707	4	US-09-740-027-3		Sequence 3, Appl
C	24	21.4	49.8	24720	4	US-09-949-016-12341		Sequence 12341, A
C	25	21.4	49.8	24721	4	US-09-949-016-15610		Sequence 15610, A
C	26	21.4	49.8	43133	4	US-09-949-016-14911		Sequence 14911, A
C	27	21.4	49.8	99498	4	US-09-949-016-12621		Sequence 12621, A

ALIGNMENTS

RESULT 1	US-09-032-297A-13	; Sequence 13, Application US/09032297A
		; Patent No. 6525184
		; GENERAL INFORMATION:
		; TITLE OF INVENTION: Self-Regulated Apoptosis of
		; RANDALL W. BARTON; Revati J. Tatake, Steven D. Marlin and
		; NUMBER OF SEQUENCES: 13
		; CORRESPONDENCE ADDRESS:
		; ADDRESSEE: Boehringer Ingelheim Corporation
		; STREET: 900 Ridgebury Road, P.O. Box 368
		; CITY: Ridgefield
		; STATE: Connecticut
		; COUNTRY: United States of America
		; ZIP: 06877-0368
		; COMPUTER READABLE FORM:
		; MEDIUM TYPE: 3.5" 1.44 Mb diskette
		; COMPUTER: IBM PC
		; OPERATING SYSTEM: MS DOS
		; SOFTWARE: Word Processing
		; CURRENT APPLICATION DATA:
		; APPLICATION NUMBER: US/09/032,297A
		; FILING DATE: 27-Feb-1998
		; CLASSIFICATION: <Unknown>
		; PRIOR APPLICATION DATA:
		; APPLICATION NUMBER: 60/038, 266
		; FILING DATE: 28-FEB-97
		; ATTORNEY/AGENT INFORMATION:
		; NAME: Robert P. Raymond
		; REGISTRATION NUMBER: 25089
		; TELECOMMUNICATION INFORMATION:
		; TELEPHONE: 203-791-6183
		; INFORMATION FOR SEQ ID NO: 13:
		; SEQUENCE CHARACTERISTICS:
		; LENGTH: 787
		; TYPE: nucleic acid
		; STRANDEDNESS: single
		; TOPOLOGY: linear
		; MOLECULE TYPE: <Unknown>
		; DESCRIPTION: DNA
		; FEATURE:
		; NAME/KEY: TNFa 3' untranslated region
		; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
		; US-09-032-297A-13
		; Query Match 100.0%; Score 43; DB 4;
		; Best Local Similarity 100.0%; Pred. No. 5.2e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 43
 Db 226 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 268

RESULT 2
 US-09-229-151C-7
 / Sequence 7, Application US/09229151C
 / Patent No. 6537784
 / GENERAL INFORMATION:
 / APPLICANT: Tatake, Revati J.
 / APPLICANT: Marlin, Steven D.
 / APPLICANT: Barton, Randall W.
 / TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
 / FILE REFERENCE: 9/137
 / CURRENT APPLICATION NUMBER: US/09/229,151C
 / CURRENT FILING DATE: 1999-01-12
 / PRIOR APPLICATION NUMBER: US 60/076,316
 / PRIOR FILING DATE: 1998-02-27
 / NUMBER OF SEQ ID NOS: 15
 / SOFTWARE: PatentIn version 2.0
 / SEQ ID NO 7
 / LENGTH: 787
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / OTHER INFORMATION: TNF-alpha untranslated region
 US-09-229-151C-7

Query Match 100.0%; Score 43; DB 4; Length 787;
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 43
 Db 226 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 268

RESULT 3
 US-09-023-655-1329
 / Sequence 1329, Application US/09023655
 / Patent No. 6607879
 / GENERAL INFORMATION:
 / APPLICANT: Cocks, Benjamin G.
 / APPLICANT: Suban G. Stuart
 / APPLICANT: Jeffrey J. Seilhamer
 / TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 / NUMBER OF SEQUENCES: 1508
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 / STREET: 3174 PORTER DRIVE
 / CITY: PALO ALTO
 / STATE: CALIFORNIA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/023,655
 / FILING DATE: HERewith
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
 / REFERENCE/DOCKET NUMBER: PA-0001 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (650) 855-0555
 / TELEFAX: (650) 845-4166
 / INFORMATION FOR SEQ ID NO: 1329:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1585 base pair**B**
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: GENBANK
 / CLONE: 9339737
 / US-09-023-655-1329

Query Match 100.0%; Score 43; DB 4; Length 1585;
 Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 43
 Db 1007 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 1049

RESULT 4
 US-09-949-016-5156
 / Sequence 5156, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / CURRENT FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SEQ ID NO 5156
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / LENGTH: 1587
 / TYPE: DNA
 / ORGANISM: Human
 / US-09-949-016-5156

Query Match 100.0%; Score 43; DB 4; Length 1587;
 Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 43
 Db 1009 TCAAACGGGCCTCCAGAAACTCACTGGGGCCTACAGCTTGA 1051

RESULT 5
 US-08-880-342-36
 / Sequence 36, Application US/08880342
 / Patent No. 6218179
 / GENERAL INFORMATION:
 / APPLICANT: Webster, Keith A.
 / APPLICANT: Bishopric, Nanette H.
 / APPLICANT: Murphy, Brian
 / APPLICANT: Laderoute, Keith R.
 / APPLICANT: Green, Christopher J.
 / TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 / TITLE OF INVENTION: Therapeutic Constructs
 / NUMBER OF SEQUENCES: 37
 / CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/880,342
 FILING DATE: 23-JUN-1997
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/IB95/00996
 FILING DATE: 13-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/365,486

FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 8255-0018.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 1643 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: TNF cDNA HSTNFR (EMBL Accession

INDIVIDUAL ISOLATE: #X01394)

FEATURE:

NAME/KEY: CDS

LOCATION: 153...851

US-08-880-342-36

Query Match 100.0%; Score 43; DB 3; Length 1643;
 Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

US-09-505-250-4

Sequence 4, Application US/09505250A

Patent No. 6329148

GENERAL INFORMATION:

APPLICANT: Rosen, Glenn

APPLICANT: Kao, Peter

TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with

Title of Invention: Triptolides and Death Domain Ligands

FILE REFERENCE: SUN-109PRV2

CURRENT APPLICATION NUMBER: US/09/505,250A

CURRENT FILING DATE: 2000-02-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 1643

TYPE: DNA

ORGANISM: H. sapiens

FEATURE:

Query Match 100.0%; Score 43; DB 4; Length 2270;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

US-09-229-151C-14

Sequence 14, Application US/09229151C

Patent No. 6537784

GENERAL INFORMATION:

APPLICANT: Tatake, Revati J.

APPLICANT: Marlin, Steven D.

APPLICANT: Barton, Randall W.

TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy

FILE REFERENCE: 9/137

CURRENT APPLICATION NUMBER: US/09/229,151C

CURRENT FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: US 60/076,316

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 2.0

SEQ ID NO 13

LENGTH: 2270

TYPE: DNA

ORGANISM: Human

FEATURE:

OTHER INFORMATION: chimeric gene : -706TNFpGB3' UTR

US-09-229-151C-13

Query Match 100.0%; Score 43; DB 4; Length 2570;

Best Local Similarity 100.0%; Pred. No. 6.6e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9

US-09-229-151C-14

Sequence 14, Application US/09229151C

Patent No. 6537784

GENERAL INFORMATION:

APPLICANT: Tatake, Revati J.

APPLICANT: Marlin, Steven D.

APPLICANT: Barton, Randall W.

TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy

FILE REFERENCE: 9/137

CURRENT APPLICATION NUMBER: US/09/229,151C

CURRENT FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: US 60/076,316

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 2.0

SEQ ID NO 14

LENGTH: 2570

TYPE: DNA

ORGANISM: Human

FEATURE:

OTHER INFORMATION: chimeric gene : -1005TNFpGB3' UTR

US-09-229-151C-14

Qy 1 TCAAACCTGGGCCCTCCAGAACTCACTGGGCCTACAGCTTGA 43
 Db 2009 TCAAACCTGGGCCCTCCAGAACTCACTGGGCCTACAGCTTGA 2051

RESULT 9
 US-09-166-186-1
 / Sequence 1, Application US/09166186A
 / Patent No. 6080580
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Brenda
 / APPLICANT: Butler, Madeline M.
 / APPLICANT: Shanahan, William R.
 / TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
 / FILE REFERENCE: ISPH-0322
 / CURRENT APPLICATION NUMBER: US/09/166,186A
 / CURRENT FILING DATE: 1998-10-05
 / NUMBER OF SEQ ID NOS: 250
 / SEQ ID NO 1
 / LENGTH: 3634
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (615)..(981)
 / FEATURE:
 / NAME/KEY: intron
 / LOCATION: (982)..(1588)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (1589)..(1634)
 / FEATURE:
 / NAME/KEY: intron
 / LOCATION: (1635)..(1821)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (1822)..(1869)
 / FEATURE:
 / NAME/KEY: intron
 / LOCATION: (1870)..(2070)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (2171)..(3381)
 / PUBLICATION INFORMATION:
 / AUTHORS: Nedwin, G.E.
 / AUTHORS: Naylor, S.L.
 / AUTHORS: Sakaguchi, A.Y.
 / AUTHORS: Smith, D.
 / AUTHORS: Jarrett-Nedwin, J.
 / AUTHORS: Pennica, D.
 / AUTHORS: Goeddel, D.V.
 / AUTHORS: Gray, P.W.
 / TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chromosomal localization
 / JOURNAL: Nucleic Acids Res.
 / VOLUME: 13
 / ISSUE: 17
 / PAGES: 6361-6373
 / DATE: 1985-09-11
 / DATABASE ACCESSION NUMBER: X02910 Genbank
 / DATABASE ENTRY DATE: 1997-02-17
 US-09-166-186-1

Query Match 100.0%; Score 43; DB 3; Length 3634;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCCTCCAGAACTCACTGGGCCTACAGCTTGA 43

RESULT 10
 US-09-313-932-1
 / Sequence 1, Application US/09313932A
 / Patent No. 6228642
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Brenda
 / APPLICANT: Bennett, C. Frank
 / APPLICANT: Butler, Madeline M.
 / APPLICANT: Shanahan, William R.
 / TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
 / FILE REFERENCE: ISPH-0356
 / CURRENT APPLICATION NUMBER: US/09/313,932A
 / CURRENT FILING DATE: 1999-05-18
 / NUMBER OF SEQ ID NOS: 501
 / SEQ ID NO 1
 / LENGTH: 3634
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (615)..(981)
 / FEATURE:
 / NAME/KEY: intron
 / LOCATION: (982)..(1588)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (1589)..(1634)
 / FEATURE:
 / NAME/KEY: intron
 / LOCATION: (1635)..(1821)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (1822)..(1869)
 / FEATURE:
 / NAME/KEY: intron
 / LOCATION: (1870)..(2070)
 / FEATURE:
 / NAME/KEY: exon
 / LOCATION: (2171)..(3381)
 / PUBLICATION INFORMATION:
 / AUTHORS: Nedwin, G.E.
 / AUTHORS: Naylor, S.L.
 / AUTHORS: Sakaguchi, A.Y.
 / AUTHORS: Smith, D.
 / AUTHORS: Jarrett-Nedwin, J.
 / AUTHORS: Pennica, D.
 / AUTHORS: Goeddel, D.V.
 / AUTHORS: Gray, P.W.
 / TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chromosomal localization
 / JOURNAL: Nucleic Acids Res.
 / VOLUME: 13
 / ISSUE: 17
 / PAGES: 6361-6373
 / DATE: 1985-09-11
 / DATABASE ACCESSION NUMBER: X02910 Genbank
 / DATABASE ENTRY DATE: 1997-02-17
 US-09-313-932-1

Query Match 100.0%; Score 43; DB 3; Length 3634;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCCCTCCAGAACTCACTGGGCCTACAGCTTGA 43

RESULT 11
 US-09-109-663-34
 ; Sequence 34, Application US/09109663
 ; GENERAL INFORMATION:
 ; APPLICANT: Tu, Guang-Chou
 ; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
 ; TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
 ; FILE REFERENCE: 9855-3U1
 ; CURRENT APPLICATION NUMBER: US/09/109,663
 ; CURRENT FILING DATE: 1998-07-03
 ; PRIOR APPLICATION NUMBER: 60/051,705
 ; EARLIER FILING DATE: 1997-07-03
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 34
 ; LENGTH: 3634
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: TNF(alpha) cDNA
 ; US-09-109-663-34

Query Match 100.0%; Score 43; DB 3; Length 3634;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAAACTCACTGGGCTTACAGCTTGA 43
 Db 2812 TCAAACGGGCCTCCAGAAACTCACTGGGCTTACAGCTTGA 2854

RESULT 12
 US-09-949-016-16898
 ; Sequence 16898, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 16898
 ; LENGTH: 6682
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-16898

Query Match 100.0%; Score 43; DB 4; Length 6682;
 Best Local Similarity 100.0%; Pred. No. 8e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACGGGCCTCCAGAAACTCACTGGGCTTACAGCTTGA 43
 Db 4103 TCAAACGGGCCTCCAGAAACTCACTGGGCTTACAGCTTGA 4145

RESULT 13
 US-09-376-774-5/C
 ; Sequence 5, Application US/09376774

RESULT 15
 US-09-949-016-15297
 ; Sequence 15297, Application US/09949016
 ; Patent No. 6812339

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; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 15297  
; LENGTH: 11865  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc_feature  
; LOCATION: (1) :i:(11865)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15297  
  
Query Match      53.5%; Score 23; DB 4; Length 11865;  
Best Local Similarity 74.4%; Pred. No. 13;  
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
Qy   1 TCAAACGTGGCCCTCCAGAACTCACTGGGGCTACAGCT 39  
Db   4740 TCCATTGGGGCCAGGCCACTGGGCTGCAGGT 4778
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Search completed: September 2, 2005, 18:55:20
Job time : 177.51 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
 Run on: September 2, 2005, 15:27:57 ; Search time 198.034 Seconds
 (without alignments)
 1421.994 Million cell updates/sec

Title: US-09-801-371A-2
 Perfect score: 43
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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Published Applications NA:
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 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB_seq:
 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB_seq:
 4: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB_seq:
 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB_seq:
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 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB_seq:
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 14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB_seq:
 15: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB_seq:
 16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB_seq:
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 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB_seq:
 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB_seq:
 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB_seq:
 22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB_seq:
 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB_seq:
 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB_seq:
 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB_seq:
 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB_seq:

 RESULT 1
 US-09-801-371A-2
 ; Sequence 2, Application US/09801371A
 ; Patent No. US20020155569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Osman, Farhat
 ; APPLICANT: Jarrous, Nayef
 ; APPLICANT: Ben-Abouli, Yitzhak
 ; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
 ; MANIPULATION OF mRNA SPLICING AND ITS USES
 ; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
 ; CURRENT APPLICATION NUMBER: US/09/801,371A
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIORITY APPLICATION NUMBER: PCT WO 00/14255
 ; PRIORITY FILING DATE: 1999-09-06
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 43
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-801-371A-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	43	9 US-09-801-371A-2	Sequence 2, Appli
c 2	43	100.0	43	9 US-09-801-371A-6	Sequence 6, Appli
3	43	100.0	50	9 US-09-801-371A-8	Sequence 8, Appli
4	43	100.0	81	9 US-09-801-371A-7	Sequence 7, Appli
5	43	100.0	104	9 US-09-801-371A-1	Sequence 1, Appli
c 6	43	100.0	104	9 US-09-801-371A-5	Sequence 5, Appli
7	43	100.0	787	18 US-10-356-308A-13	Sequence 13, Appli

Query Match 100.0%; Score 43; DB 9; Length 43;
 Best Local Similarity 100.0%; Pred. No. 8e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCAAACTGGGCCCTCCAGAACTCACTGGGGCTACAGCTTGA 43

```

; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF mRNA SPlicing AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
; US-09-801-371A-7

Query Match 100.0%; Score 43; DB 9; Length 81;
Best Local Similarity 79.1%; Pred. No. 8e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
; General Information:
Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 43
Db 9 UCAAACUGGGCCUCCAGAACUCACUGGGCCUACAGCUUGA 51

; General Information:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF mRNA SPlicing AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-801-371A-6

Query Match 100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; General Information:
Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 43
Db 43 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 1

; General Information:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF mRNA SPlicing AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-371A-1

Query Match 100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; General Information:
Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 43
Db 5 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 47

; General Information:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF mRNA SPlicing AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
; US-09-801-371A-8

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Best Local Similarity 79.1%; Pred. No. 8e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
; General Information:
Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 43
Db 5 UCAAACUGGGCCUCCAGAACUCACUGGGCCUACAGCUUGA 47

; General Information:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF mRNA SPlicing AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-371A-5/C

Query Match 100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; General Information:
Qy 1 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 43
Db 5 TCAAACGGGCCTCCAGAACTCACTGGGCCAACAGCTTGA 47

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; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5

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Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Length: 798

Qy 1 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
Db 100 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 58

RESULT 7
US-10-356-308A-13
; Sequence 13, Application US/10356308A
; Publication No. US20040039186A1
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall Wilber
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/121-1-CIP1
; CURRENT APPLICATION NUMBER: US/10/356,308A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/032,297
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 1 to 787
; OTHER INFORMATION: TNFa 3' untranslated region
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E., et al.
; JOURNAL: Nucleic Acid Research
; VOLUME: 13
; PAGES: 6361-6373
; DATE: 1995
; US-10-356-308A-13

Query Match 100.0%; Score 43; DB 9; Length 787;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Length: 798

Qy 1 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
Db 226 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 268

RESULT 8
US-10-895-393-9
; Sequence 9, Application US/10895393
; Publication No. US20050048549A1
; GENERAL INFORMATION:
; APPLICANT: CAO, Liangxian
; APPLICANT: MEHTA, Anuradha
; APPLICANT: NARYSHKIN, Nikolai A.
; APPLICANT: PELLEGRINI, Matthew C.

Query Match 100.0%; Score 43; DB 20; Length 806;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Length: 806

Qy 1 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
Db 221 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 273

RESULT 9
US-10-814-634A-5
; Sequence 5, Application US/10814634A
; Publication No. US20040231007A1
; GENERAL INFORMATION:
; APPLICANT: KASTELIC, Tania
; APPLICANT: Novation Pharmaceuticals Inc.
; TITLE OF INVENTION: Assay for Identifying Compounds Which
; FILE REFERENCE: 793-104CIP
; CURRENT APPLICATION NUMBER: US/10/814,634A
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 09/869,159
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: GB 9828709.7
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 5
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-814-634A-5

Query Match 100.0%; Score 43; DB 20; Length 806;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Length: 806

Qy 1 TCAAACCTGGGCCTCCAGAACCTCACTGGGCCTACAGCTTGA 43
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; / APPLICANT: Kaser, Matthew R.
; / TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; / FILE REFERENCE: PA-0050 US
; / CURRENT APPLICATION NUMBER: US/10/247,671
; / CURRENT FILING DATE: 2002-09-18
; / PRIOR APPLICATION NUMBER: 60/323,784
; / PRIOR FILING DATE: 2001-09-19
; / NUMBER OF SEQ ID NOS: 186
; / SOFTWARE: PERL Program
; / SEQ ID NO 120
; / LENGTH: 1279
; / TYPE: DNA
; / ORGANISM: Homo sapiens
; / FEATURE:
; / NAME/KEY: misc_feature
; / OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
US-10-247-671-120

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Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1081 TCAAACGGGCCTCCAGAACACTGGGCCTACAGCTTGA 1123

RESULT 11
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; / APPLICANT: Dai, Hongyue
; / APPLICANT: He, Yudong
; / APPLICANT: Linsley, Peter
; / APPLICANT: Mao, Mao
; / APPLICANT: Roberts, Peter
; / APPLICANT: Van 't Veer, Laura
; / APPLICANT: Van de Vijver, Marc
; / APPLICANT: Bernards, Rene
; / TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; / FILE REFERENCE: 9301-175-999
; / CURRENT APPLICATION NUMBER: US/10/172,118
; / CURRENT FILING DATE: 2002-06-14
; / PRIOR APPLICATION NUMBER: 60/380,770
; / PRIOR FILING DATE: 2002-05-14
; / NUMBER OF SEQ ID NOS: 2699
; / SEQ ID NO 501
; / LENGTH: 1585
; / TYPE: DNA
; / ORGANISM: Homo sapiens
; / PUBLICATION INFORMATION:
; / DATABASE ACCESSION NUMBER: NM_000594
; / DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501

Query Match 100.0%; Score 43; DB 17; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1007 TCAAACGGGCCTCCAGAACACTGGGCCTACAGCTTGA 1049

RESULT 12
US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; / APPLICANT: Dai, Hongyue
; / APPLICANT: He, Yudong
; / APPLICANT: Linsley, Peter S.
; / APPLICANT: Mao, Mao
; / APPLICANT: Roberts, Peter
; / APPLICANT: Van 't Veer, Laura
; / APPLICANT: Van de Vijver, Marc
; / APPLICANT: Bernards, Rene
; / TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; / FILE REFERENCE: 9301-188-999
; / CURRENT APPLICATION NUMBER: US/10/342,887
; / CURRENT FILING DATE: 2003-01-15
; / PRIOR APPLICATION NUMBER: 60/298,918
; / PRIOR FILING DATE: 2001-06-18
; / PRIOR APPLICATION NUMBER: 60/380,710
; / PRIOR FILING DATE: 2002-05-14
; / PRIOR APPLICATION NUMBER: 10/172,118
; / PRIOR FILING DATE: 2002-06-14
; / NUMBER OF SEQ ID NOS: 2699
; / SEQ ID NO 501
; / LENGTH: 1585
; / TYPE: DNA
; / ORGANISM: Homo sapiens
; / PUBLICATION INFORMATION:
; / DATABASE ACCESSION NUMBER: US2004007703A1
; / GENERAL INFORMATION:
; / APPLICANT: Cocks, Benjamin G.
; / APPLICANT: Susan G. Stuart
; / APPLICANT: Jeffrey J. Seilhamer
; / TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; / GENE EXPRESSION
; / NUMBER OF SEQUENCES: 1508
; / CORRESPONDENCE ADDRESS:
; / ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; / STREET: 3174 PORTER DRIVE
; / CITY: PALO ALTO
; / STATE: CALIFORNIA
; / COUNTRY: USA
; / ZIP: 94304
; / COMPUTER READABLE FORM:
; / MEDIUM TYPE: Floppy disk
; / COMPUTER: IBM PC compatible
; / OPERATING SYSTEM: PC-DOS/MS-DOS
; / SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; / CURRENT APPLICATION DATA:
; / APPLICATION NUMBER: US/10/641,643
; / FILING DATE: 14-Aug-2003
; / CLASSIFICATION: <Unknown>
; / PRIOR APPLICATION DATA:
; / APPLICATION NUMBER: <Unknown>
; / FILING DATE: <Unknown>
; / ATTORNEY/AGENT INFORMATION:
; / NAME: Zeller, Karen J.
; / REGISTRATION NUMBER: 37,071
; / TELECOMMUNICATION INFORMATION:
; / REFERENCE/DOCKET NUMBER: PA-0001 US
; / TELEPHONE: (650) 855-0555
; / TELEFAX: (650) 845-4166
; / INFORMATION FOR SEQ ID NO: 1329:
; / SEQUENCE CHARACTERISTICS:
; / LENGTH: 1585 base pairs
; / TYPE: nucleic acid
; / STRANDEDNESS: single

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; TOPOLGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9339737
; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329

Query Match      100.0%; Score 43; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; PUBLICATION INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10370715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
SEQ ID NO 19
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-19

RESULT 14
US-10-370-715B-19
; Sequence 19, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
SEQ ID NO 19
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-19

Query Match      100.0%; Score 43; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Db          1074 TCAAACCTGGGCCTCCAGAACTCACTGGGCCCTACAGCTTTGA 1116
; RELEVANT RESIDUES: (1) .. (1643)
; US-10-272-411-4

Query Match      100.0%; Score 43; DB 15; Length 1643;
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; RELEVANT RESIDUES: (1) .. (1643)
; US-10-272-411-4

Search completed: September 3, 2005, 00:21:56
Job time : 198.034 secs

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